

AGC TCC ACC GCG GTG GCG GCC GCT CTA GAA CTA GTG GAT CCC CCG GGC Ser Ser Thr Ala Val Ala Ala Ala Leu Glu Leu Val Asp Pro Pro Gly	48
TGC AGG AAT TCG GCA CGA GCC GAT CTC GGT GCC GAC CGC CTC TCC AAG Cys Arg Asn Ser Ala Arg Ala Asp Leu Gly Ala Asp Arg Leu Ser Lys	96
ATC GAC AAG GAG AGA GCC GGA GTG CTG GTC GGA ACA GGA ATG GGT GGT Ile Asp Lys Glu Arg Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly	144
CTG ACT GTC TTC TCT GAC GGG GTT CAG TCT CTT ATC GAG AAG GGT CAC Leu Thr Val Phe Ser Asp Gly Val Gln Ser Leu Ile Glu Lys Gly His	192
CGG AAA ATC ACC CCT TTC TTC ATC CCC TAT GCC ATT ACA AAC ATG GGG Arg Lys Ile Thr Pro Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly	240
TCT GCC CTG CTC GCT ATC GAA TTT GGT CTC ATG GGC CCA AAC TAT TCA Ser Ala Leu Leu Ala Ile Glu Phe Gly Leu Met Gly Pro Asn Tyr Ser	288
AAT TCC ACT GCA TGT GCC ACT TCC AAC TAC TGC TTC CAT GCT GCC GCT Ile Ser Thr Ala Cys Ala Thr Ser Ser Asn Tyr Cys Phe His Ala Ala Ala	336
AAT CAT ATC CGC CGT GGT GAG GCT GAT CTT ATG ATT GCT GGA GGC ACT Asn His Ile Arg Arg Gly Glu Ala Asp Leu Met Ile Ala Gly Gly Thr	384

FIGURE 1
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GAG GCC GCA ATC ATT CCA ATT GGG TTG GGA GGC TTT GTG GCT TGC AGG Glu Ala Ala Ile Ile Pro Ile Gly Leu Gly Phe Val Ala Cys Arg	432
GCT TTG TCT CAA AGG AAC GAT GAC CCG CAG ACT GCC TCT AGG CCC TGG Ala Leu Ser Gln Arg Asn Asp Pro Gln Thr Ala Ser Arg Pro Trp	480
GAT AAA GAC CGT GAT GGT TTT GTG ATG GGT GAA GGT GCT GGA GTG TTG Asp Lys Asp Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu	528
GTG ATG GAG AGC TTG GAA CAT GCA ATG AGA CGA GGA GCA CCG ATT ATT Val Met Glu Ser Leu Glu His Ala Met Arg Arg Gly Ala Pro Ile Ile	576
GCA GAG TAT TTG GGA GGT GCA ATC AAC TGT GAT GCT TAT CAC ATG ACT Ala Glu Tyr Leu Gly Gly Ala Ile Asn Cys Asp Ala Tyr His Met Thr	624
GAT CCA AGG GCT GAT GGT CTT GGT GTC TCT TCT TGC ATT GAG AGT AGC Asp Pro Arg Ala Asp Gly Leu Gly Val Ser Ser Cys Ile Glu Ser Ser	672
CTT GAA GAT GCT GGC GTC TCA CCT GAA GAG GTC AAT TAC ATA AAT GCT Leu Glu Asp Ala Gly Val Ser Pro Glu Glu Val Asn Tyr Ile Asn Ala	720

FIGURE 1
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CAT GCG ACT TCT ACT CTA GCT GGG GAT CTC GCC GAG ATA AAT GCC ATC His Ala Thr Ser Thr Leu Ala Gly Asp Leu Ala Glu Ile Asn Ala Ile	768
AAG AAG GGT TTC AAG AAC ACA AAG GAT ATC AAA ATT AAT GCA ACT AAG Lys Lys Val Phe Lys Asn Thr Lys Asp Ile Lys Ile Asn Ala Thr Lys	816
TCA ATG ATC GGA CAC TGT CTT GGA GCA TCT GGA GGT CTT GAA GCT ATA Ser Met Ile Gly His Cys Leu Gly Ala Ser Gly Gly Leu Glu Ala Ile	864
GCG ACT ATT AAG GGA ATA AAC ACC GGC TGG CTT CAT CCC AGC ATT AAT Ala Thr Ile Lys Gly Ile Asn Thr Gly Trp Leu His Pro Ser Ile Asn	912
CAA TTC AAT CCT GAG CCA TCG GTG GAG TTC GAC ACT GTT GCC AAC AAG Gln Phe Asn Pro Glu Pro Ser Val Glu Phe Asp Thr Val Ala Asn Lys	960
AAG CAG CAA CAC GAA GTT AAC GTT GCG ATC TCG AAT TCA TTC GGA TTT Lys Gln Gln His Glu Val Asn Val Ala Ile Ser Asn Ser Phe Gly Phe	1008
GGA GGC CAC AAC TCA GTC GTG GCT TTC TCG GCT TTC AAG CCA TGA TTA Gly Gly His Asn Ser Val Val Ala Phe Ser Ala Phe Lys Pro	1056

FIGURE 1
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CCCA'TTTCAC	AGG'TACTTG	TCATTGAGAA	T'ACGGATTAT'	GGACTTGCAG	AGTAA'TTTC	1116
CCATGTTTGT	CGGAGAGACA	TAT'TACCCAG	GTTG'I'CCG'IC	AAACCCAT'T'	AGGAT'AC'IGT'	1176
'TCTATGTAAAT	AAAC'ATAAG	ATTAT'TTAAAT'	TCCC'TT'TTAA	TCCIGTC'ICC	AG'ITTGAGCA	1236
TGAATTTATA	TTTATTTTAT	C'TTAGAAAGG	TCAAA'TAAGA	TTT'IGT'TTAA	CCTCTGTAAA	1296
ACTTTTGTTT	GTATTGGAAA	GGAAGTGCCG	TCTCAAAAAA	AAAAAA'AAA	AA	1348

FIGURE 1
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Sequence Range: 1 to 1704

AAA TTA ACC CTC ACT AAA GGG AAC AAA AGC TGG AGC TCC ACC GNG GTG	10	20	30	40
Lys Leu Thr Leu Thr Lys Gly Asn Lys Ser Trp Ser Ser Thr Xxx Val>				
50	60	70	80	90
CGG GCC GCT CTA GAA CTA GTG GAT CCC CCG GGC TGC AGG AAT TCG GCA				
Ala Ala Ala Leu Glu Leu Val Asp Pro Pro Gly Cys Arg Asn Ser Ala>				
100	110	120	130	140
CGA GCC GGC ATG GGC CTC GTC TCC GTA TTC GGC TCC GAC GTC GAC TCT				
Arg Ala Gly Met Gly Leu Val Ser Val Phe Gly Ser Asp Val Asp Ser>				
150	160	170	180	190
TAT TAC GAA AAG CTC CTC TCC GGC GAG AGC GGG ATC AGC TTA ATC GAC				
Tyr Tyr Glu Lys Lys Leu Ser Gly Glu Ser Gly Ile Ser Leu Ile Asp>				
200	210	220	230	240
CGC TTC GAC GCT TCC AAG TTC CCC ACC AGG TTC GGC GGC CAG ATC CGG				
Arg Phe Asp Ala Ser Lys Phe Pro Thr Arg Phe Gly Gly Gln Ile Arg>				
250	260	270	280	
GGA TTC AAC GCG ACG GGA TAC ATC GAC GGG AAG AAC GAC AGG AGG CTC				
Gly Phe Asn Ala Thr Gly Tyr Ile Asp Gly Lys Asn Asp Arg Arg Leu>				
300	310	320	330	
GAC GAT TGC CTC CGC TAC TGC ATT GTC GCC GGG AAG AAG GCT CTC GAA				
Asp Asp Cys Leu Arg Tyr Cys Ile Val Ala Gly Lys Lys Ala Leu Glu>				

FIGURE 2
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340	350	360	370	380
AMT TCC GAT CTC GGC GGT GAA AGC CTC TCC AAG ATT GAT AAG GAG AGA				
Asn Ser Asp Leu Gly Gly Ser Leu Ser Lys Ile Asp Lys Glu Arg>				
390	400	410	420	430
GCT GGA GTG CTA GTT GGA ACT GGT ATG GGT GGC CTA ACC GTC TTC TCT				
Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly Leu Thr Val Phe Ser>				
440	450	460	470	480
GAC GGG GTT CAG AMT CTC ATC GAG AAA GGT CAC CGG AAG ATC TCC CCG				
Asp Gly Val Gln Asn Leu Ile Glu Lys Gly His Arg Lys Ile Ser Pro>				
490	500	510	520	
TTT TTC ATT CCC TAT GCC ATT ACA AAC AAG GGG TCT GCT CTG CTT GCC				
Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly Ser Ala Leu Leu Ala>				
30	540	550	560	570
ATC GAT TTG GGT CTG ATG GGC CCA AAC TAT TCG ATT TCA ACT GCA TGT				
Ile Asp Leu Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys>				
580	590	600	610	620
GCT ACT TCC AAC TAC TGC TTT TAT GCC GCT GCC AAT CAT ATC CGC CGA				
Ala Thr Ser Asn Tyr Cys Phe Tyr Ala Ala Ala Asn His Ile Arg Arg>				
630	640	650	660	670
GGC GAG GCT GAC CTC ATG ATT GCT GGA GGA ACT GAG GCT GCA ATC ATT				
Gly Glu Ala Ala Asp Leu Met Ile Ala Gly Gly Thr Glu Ala Ala Ile Ile>				

FIGURE 2
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680	690	700	710	720
CCA AAT GGG TTA GGA TTC GTT GCC TGC AGG GCT TTA TCT CAA AGG				*
Pro Ile Gly Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg>				
	730	740	750	760
AAT GAT GAC CCT CAG ACT GCC TCA AGG CCG TGG GAT AAG GAC CGT GAT				
Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp Asp Lys Asp Arg Asp>				
70	780	790	800	810
	*			
GGT TTT GTG ATG GGC GNA GGG GCT GGA GTA TTG GTT ATG GAG AGC TTG				
Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Val Met Glu Ser Leu>				
820	830	840	850	860
GAA CAT GCA ATG AAA CGA GGA GCG CCG AAT ATT GCA GAA TAT TTG GGA				
Glu His Ala Met Lys Arg Gly Ala Pro Ile Ile Ala Glu Tyr Leu Gly>				
870	880	890	900	910
GGT GCA GTC AAT TGT GAT GCT TAT CAT ATG ACT GAT CCA AGG GCT GAT			*	
Gly Ala Val Asn Cys Asp Ala Tyr His Met Thr Asp Pro Arg Ala Asp>				
920	930	940	950	960
GGG CTT GGT GTC TCC TCT TGC ATT GAG AGC AGT CTG GAA GAT GCT GGG				*
Gly Leu Gly Val Ser Ser Cys Ile Glu Ser Ser Leu Glu Asp Ala Gly>				
	970	980	990	1000
GTC TCA CCT GAA GAG GTC AAT TAC ATA AAT GCT CAT CCG ACT TCC ACT				
Val Ser Pro Glu Glu Val Asn Tyr Ile Asn Ala His Ala Thr Ser Thr>				

FIGURE 2
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10	1020	1030	1040	1050
CTT GCT GGG GAT CTT GCC GAG ATA AAT GCC ATC AAG AAG GTT TTC AAG				
Leu Ala Gly Asp Leu Ala Glu Ile Asn Ala Ile Lys Lys Val Phe Lys>				
1060	1070	1080	1090	1100
AAC ACC AAG GAA ATC ACA ATC AAT GCA ACT AAG TCG ATG ATC GGA CAC				
Asn Thr Lys Glu Ile Thr Ile Asn Ala Thr Lys Ser Met Ile Gly His>				
1110	1120	1130	1140	1150
TGT CTT GGA GCA TCA GGG GGT CTT GAA GCC ATT GCG ACA ATT AAG GGA				
Cys Leu Gly Ala Ser Gly Gly Leu Glu Ala Ile Ala Thr Ile Lys Gly>				
1160	1170	1180	1190	1200
ATA ACC ACC GGC TGG CTT CTT CCC AGC ATA AAC CAA TTC AAT CCC GAG				
Ile Thr Thr Gly Trp Leu His Pro Ser Ile Asn Gln Phe Asn Pro Glu>				
1210	1220	1230	1240	
CCA TCA GTG GAA TTC GAC ACA GTT GCC AAC AAG AAG CAG CAA CAT GAA				
Pro Ser Val Glu Phe Asp Thr Val Ala Asn Lys Lys Gln Gln His Glu>				
50	1260	1270	1280	1290
GTG AAT GTT GCT ATC TCA AAT TCA TTC GGA TTC GGA GGC CAC AAC TCA				
Val Asn Val Ala Ile Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser>				
1300	1310	1320	1330	1340
GTT GTA GCT TTC TCA GCC TTC AAG CCA TGA TTA CTC GGT TCA AAT GCA				
Val Val Ala Phe Ser Ala Phe Lys Pro				

FIGURE 2
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Sequence Range: 1 to 2046

10	20	30	40	50	60
ACTAAAGGGA ACAAAAGCTG GAGCTCCACC GCGGTGGCGG CCGCTCTAGA ACTAGTGGAT *					
70	80	90	100	110	120
CCCCCGGGCT GCAGGAATTC GGCACGAGTT TTCTTACTTG GGTGGGCTCA GTCAGGCTGT					
130	140	150	160		
TCCA ATG GCG ACC GCT TCT TGC ATG GAT GCG TCC CCT TTC TGT ACG TGG					
Met Ala Thr Ala Ser Cys Met Val Ala Ser Pro Phe Cys Thr Trp					
170	180	190	200	210	
CTC GTA GCT GCA TGC ATG CCC ACT TCA TCC GAC AAC GAC CCA CGT TCC					
Leu Val Ala Ala Cys Met Pro Thr Ser Ser Asp Asn Asp Pro Arg Ser					
220	230	240	250	260	
CTT TCC CAC AAG CCG CTC CGC CTC TCC CGT CGC CGG AGG ACT CTC TCC					
Leu Ser His Lys Arg Leu Arg Leu Ser Arg Arg Arg Thr Leu Ser					
270	280	290	300	310	
TCC CAT TGC TCC CTC CGC GGA TCC ACC TTC CAA TGC CTC GAT CCT TGC					
Ser His Cys Ser Leu Arg Gly Ser Thr Phe Gln Cys Leu Asp Pro Cys					
320	330	340	350	360	
AAC CAG CAA CGC TTC CTC GGG GAT AAC GGA TTC GGT TCC CTC TTC GGA					
Asn Gln Gln Arg Phe Leu Gly Asp Asn Gly Phe Ala Ser Leu Phe Gly					

FIGURE 3
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370	TCC AAG CCT CTT CGT TCA AAT CGC GGC CAC CTG AGG CTC GGC CGC ACT	380	390	400
	Ser Lys Pro Leu Arg Ser Asn Arg Gly His Leu Arg Leu Gly Arg Thr			
410	420	430	440	450
	TCC CAT TCC GGG GAG GTC ATG GCT GTG GCT ATG CAA CCT GCA CAG GAA			
	Ser His Ser Gly Glu Val Met Ala Val Ala Met Gln Pro Ala Gln Glu			
460	470	480	490	500
	GTC TCC ACA AAT AAG AAA CCT CCT ACC AAG CAA AGG CGA GTA GTT GTG			
	Val Ser Thr Asn Lys Lys Pro Ala Thr Lys Gln Arg Arg Val Val Val			
510	520	530	540	550
	ACA GGT ATG GGC GTG GTG ACT CCT CTA GGC CAT GAC CCC GAT GTT TAC			
	Thr Gly Met Gly Val Val Thr Pro Leu Gly His Asp Pro Asp Val Tyr			
560	570	580	590	600
	TAC AAC AAT CTC CTA GAC GGA ATA AGT GGC ATA AGT GAG ATA GAG AAC			
	Tyr Asn Asn Leu Leu Asp Gly Ile Ser Gly Ile Ser Glu Ile Glu Asn			
610	620	630	640	
	TTC GAC TGC TCT CAG TTT CCC ACG AGA ATT GCC GGA GAG ATC AAG TCT			
	Phe Asp Cys Ser Gln Phe Pro Thr Arg Ile Ala Gly Glu Ile Lys Ser			
650	660	670	680	690
	TTT TCC ACA GAT GGC TGG GTG GCC CCA AAG TTC TCC GAG AGG ATG GAC			
	Phe Ser Thr Asp Gly Trp Val Ala Pro Lys Phe Ser Glu Arg Met Asp			

FIGURE 3
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700		710	720	730	740
AAG TTC ATG CTT	TAC ATG CTG ACT	GCA GGC AAG AAA GCA TTA GCA GAT			
Lys Phe Met Leu Tyr Met Leu Thr Ala Gly Lys Ala Leu Ala Asp					
750	760	770	780	790	
GGT GCA ATC ACT GAA GAT GCG ATG AAA GAG CTC AAT AAA AGA AAG TGT					
Gly Gly Ile Thr Glu Asp Ala Met Lys Glu Leu Asn Lys Arg Lys Cys					
800	810	820	830	840	
GGA GTT CTC ATT GGC TCC GGA TTG GGC GGT ATG AAG GTA TTC AGC GAT					
Gly Val Leu Ile Gly Ser Gly Leu Gly Gly Met Lys Val Phe Ser Asp					
850	860	870	880		
TCC ATT GAA GCT CTG AGG ACT TCA TAT AAG AAG ATC AGT CCC TTT TGT					
Ser Ile Glu Ala Leu Arg Thr Ser Tyr Lys Lys Ile Ser Pro Phe Cys					
890	900	910	920	930	
GTA CCT TTT TCT ACC ACA AAT ATG GGA TCC GCT ATT CTT GCA ATG GAC					
Val Pro Phe Ser Thr Thr Asn Met Gly Ser Ala Ile Leu Ala Met Asp					
940	950	960	970	980	
TTG GGA TGG ATG GGC CCT AAC TAT TCG ATA TCA ACT GCC TGT GCA ACA					
Leu Gly Trp Met Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr					

FIGURE 3
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990	1000	1010	1020	1030
AGT AAC TTC TGT ATA CTG AAT GCT GCG AAC CAC ATA ATC AAA GGC GAA			*	
Ser Asn Phe Cys Ile Leu Asn Ala Ala Asn His Ile Ile Lys Gly Glu				
1040	1050	1060	1070	1080
GCA GAC ATG ATG CTT TGT GGT GGC TCG GAT GCG GCC GTT TTA CCT GTT				*
Ala Asp Met Met Leu Cys Gly Gly Ser Asp Ala Ala Val Leu Pro Val				
1090	1100	1110	1120	
GGT TTG GGA GGT TTC GTA GCA TGC CGA GCT TTG TCA CAG AGG AAT AAT				
Gly Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg Asn Asn				
1130	1140	1150	1160	1170
	*			
GAC CCT ACC AAA GCT TCG AGA CCA TGG GAC AGT AAT CGT GAT GGA TTT				
Asp Pro Thr Lys Ala Ser Arg Pro Trp Asp Ser Asn Arg Asp Gly Phe				
1180	1190	1200	1210	1220
		*		
GTG ATG GGA GAA GGA GCT GGA GGT TTA CTT CTT GAG GAG TTA GAG CAT				
Val Met Gly Glu Gly Ala Gly Val Leu Leu Leu Glu Glu Leu Glu His				
1230	1240	1250	1260	1270
			*	
GCA AAG AAA AGA GGT GCA ACC ATT TAT GCG GAA TTT CTA GGT GGG AGT				
Ala Lys Lys Arg Gly Ala Thr Ile Tyr Ala Glu Phe Leu Gly Gly Ser				
1280	1290	1300	1310	1320
				*
TTC ACT TGC GAC GCC TAC CAC ATG ACC GAG CCT CAC CCT GAA GGA GCT				
Phe Thr Cys Asp Ala Tyr His Met Thr Glu Pro His Pro Glu Gly Ala				

FIGURE 3
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1330	1340	1350	1360
GGT GTG ATC CTC TGC ATA GAG AAG GCC TTG GCT CAG TCC GGA GTC TCG			
Gly Val Ile Leu Cys Ile Glu Lys Ala Leu Ala Gln Ser Gly Val Ser			
1370	1380	1390	1400
			1410
AGG GAA GAC GTA AAT TAC ATA AAT GCG CAT GCA ACT TCC ACT CCT GCT			
Arg Glu Asp Val Asn Tyr Ile Asn Ala His Ala Thr Ser Thr Pro Ala			
1420	1430	1440	1450
			1460
GGA GAT ATC AAG GAA TAC CAA GCT CTC GCC CAC TGT TTC GGC CAA AAC			
Gly Asp Ile Lys Glu Tyr Gln Ala Leu Ala His Cys Phe Gly Gln Asn			
1470	1480	1490	1500
			1510
AGT GAG CTG AGA GTG AAT TCC ACC AAA TCG ATG ATC GGT CAC CTT CTT			
Ser Glu Leu Arg Val Asn Ser Thr Lys Ser Met Ile Gly His Leu Leu			
1520	1530	1540	1550
			1560
GGA GGA GCT GGT GGC GTA GAA GCA GTT GCA GTA GTT CAG GCA ATA AGG			
Gly Gly Ala Gly Gly Val Glu Ala Val Ala Val Val Gln Ala Ile Arg			
1570	1580	1590	1600
ACA GGA TGG ATC CAT CCA AAT ATT AAT TTG GAA GAC CCG GAC GAA GGC			
Thr Gly Trp Ile His Pro Asn Ile Asn Leu Glu Asp Pro Asp Glu Gly			
1610	1620	1630	1640
			1650
GTG GAT GCA AAA CTG CTC GTC GGC CCT AAG AAG GAG AAA CTG AAG GTC			
Val Asp Ala Lys Lys Leu Leu Val Gly Pro Lys Lys Glu Lys Leu Lys Val			

FIGURE 3
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1660	1670	1680	1690	1700
<p> AAG GTC GGT TTG TCC AAT TCA TTT GGG TTC GGC GGC CAT AAC TCA TCC Lys Val Gly Leu Ser Asn Ser Phe Gly Phe Gly His Asn Ser Ser </p>				
1710	1720	1730	1740	1750
<p> ATA CTA TTT GCC CCC TGC AAC TAG A AAAGAGTCIG TGGAAAGCCGA GAGTCTTTTGA Ile Leu Phe Ala Pro Cys Asn *** </p>				
1770	1780	1790	1800	1810
<p> GAACTCATGC ACGTTAGTAG CTTCTTTATGC CTCTGNAACC GAGATAGACC GGCTACTCGA </p>				
1830	1840	1850	1860	1870
<p> GGGGATGCCA AAGATACTCC TTGCCGGTAT TGGTGTTAAG AGATCACTGC TTGTCCCCTTT </p>				
1890	1900	1910	1920	1930
<p> TATTTTCTTC TTCTTTTGAG AGCITTAAACC GAGGTAGTCG TATTTTCGAG CTTTTCGAAAT </p>				
1950	1960	1970	1980	1990
<p> ACATGTTCGT TATCGGATCA ATGIGTTTCT TCTAAGATCA TTGTAAATGC ATATTTTGA </p>				
2010	2020	2030	2040	
<p> AAACCAACATC TCAGTATGCA AAATAAAAAA AAAAAAAAAA AAAAAA </p>				

FIGURE 3
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Sequence Range: 1 to 1921

10	20	30	40	50	60
CGGCACGAGG TCACCTCTTA CCTCGCCTGC TTCGAGCCCT GCCATGACTA CTACACCTCC					
70	80	90	100	110	120
GCATCCTTGT TCGGATCCAG GCCCATCCGC ACCACCCGCA GGCACCGGAG GCTCAATCGA					
130	140	150	160	170	180
GCTTCCCTT CCGGGGAGG AATGGCTGTG GCTCTGCAC CAGCACAGGA AGTTACCA					
190	200	210	220		
AAG AAG AAG CCA AGT ATC AAA CAG CGG CGA GTA GTT GTG ACT GGA ATG					
Lys Lys Lys Pro Ser Ile Lys Lys Gln Arg Arg Val Val Val Thr Gly Met>					
230	240	250	260	270	
GGT GTG GTG ACT CCT CTA GGC CAT GAC CCT GAT GTT TTC TAC AAT AAT					
Gly Val Val Thr Pro Leu Gly His Asp Pro Asp Val Phe Tyr Asn Asn>					
280	290	300	310	320	
CTG CTT GAT GGA ACG AGT GGC ATA AGT GAG ATA GAG ACC TTT GAT TGT					
Leu Leu Asp Gly Thr Ser Gly Ile Ser Glu Ile Glu Thr Phe Asp Cys>					
330	340	350	360	370	
GCT CAA TTT CCT ACG AGA ATT GCT GGA GAG ATC AAG TCT TTC TCC ACA					
Ala Gln Phe Pro Thr Arg Ile Ala Gly Glu Ile Lys Ser Phe Ser Thr>					

FIGURE 4
1/6

380	390	400	410	420
GAT	GGT	TGG	GTG	GCC
CCG	AAG	CTC	TCC	AAG
AGG	ATG	GAC	AAG	TTC
ATG	ATG	ATG	GAC	ATG
Asp	Gly	Trp	Val	Ala
Pro	Lys	Ser	Lys	Arg
Met	Asp	Met	Asp	Lys
Phe	Met			
Met				
430	440	450	460	
CTT	TAC	ATG	CTG	ACT
GCC	AAG	AAA	GCA	TTA
ACA	TAA	GAT	GGA	ATC
Leu	Tyr	Met	Leu	Thr
Ala	Gly	Lys	Ala	Leu
Thr	Asn	Gly	Ile	
470	480	490	500	510
ACC	GAA	GAT	GTG	ATG
AAA	GAG	CTA	GAT	AAA
AGA	AAA	TGC	GGA	GTT
CTC	Thr	Glu	Asp	Val
Leu	Met	Lys	Arg	Lys
Cys	Gly	Val	Leu	
520	530	540	550	560
ATT	GGC	TCA	GCA	ATG
GGT	GGA	ATG	ATG	GTA
TTC	AAA	GAT	GCC	ATT
GAA	Ile	Gly	Ser	Ala
Met	Ala	Met	Gly	Met
Lys	Met	Lys	Val	Phe
Asn	Pro	Phe	Asn	Asp
Ala	Ile	Glu		
570	580	590	600	610
GCC	CTA	AGG	ATT	TCA
TAA	TAA	AAG	AAG	ATG
AAA	CCC	TAT	TGT	GTA
CCT	TTC	Ala	Leu	Arg
Ile	Arg	Ile	Ser	Tyr
Lys	Met	Asn	Pro	Phe
Cys	Val	Pro	Phe	
620	630	640	650	660
GCT	ACC	ACA	AAT	ATG
GGA	TCA	GCT	ATG	CTT
GCA	ATG	GAC	TTG	GGA
TGG	Ala	Thr	Thr	Asn
Met	Gly	Ser	Ala	Met
Leu	Ala	Met	Asp	Leu
Gly	Trp			
670	680	690	700	
ATG	GGC	CCC	AAC	TAC
TCG	ATA	TCT	ACT	GCT
TGT	GCA	ACG	AGT	AAC
TTT	Met	Gly	Pro	Asn
Tyr	Ser	Ile	Ser	Thr
Ala	Cys	Ala	Thr	Ser
Asn	Phe			

FIGURE 4
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710	720	730	740	750
TGT ATC CTG AAT GCT GCG AAC CAC ATA ATC AGA GGC GAA GCA GAT GTG				
Cys Ile Leu Asn Ala Ala Asn His Ile Ile Arg Gly Glu Ala Asp Val>				
760	770	780	790	800
ATG CTT TGC GGG GGC TCA GAT GCG GTA ATC ATA CCT ATT GGT ATG GGA				
Met Leu Cys Gly Gly Ser Asp Ala Val Ile Ile Pro Ile Gly Met Gly>				
810	820	830	840	850
GGT TTT GTT GCA TGC CGA GCT TTG TCA CAG AGA AAT GCC GAC CCT ACT				
Gly Phe Val Ala Cys Arg Ala Leu Ser Gln Arg Asn Ala Asp Pro Thr>				
860	870	880	890	900
AAA GCT TCA AGA CCA TGG GAC AGT AAT CGT GAT GGA TTT GTT ATG GGG				
Lys Ala Ser Arg Pro Trp Asp Ser Asn Arg Asp Gly Phe Val Met Gly>				
910	920	930	940	
GAA GGA GCT GGA GTG CTA CTA CTA GAG GAG TTA GAG CAT GCA AAG AAA				
Glu Gly Ala Gly Val Leu Leu Leu Leu Glu Glu Leu Glu His Ala Lys Lys>				
950	960	970	980	990
AGA GGT GCG ACT ATT TAC GCA GAA TTT CTA GGT GGA AGT TTC ACT TGC				
Arg Gly Ala Thr Ile Tyr Ala Glu Phe Leu Gly Gly Ser Phe Thr Cys>				
1000	1010	1020	1030	1040
GAT GCC TAC CAC ATG ACC GAG CCT CAC CCT GAT GGA GCT GGA GTG ATT				
Asp Ala Tyr His Met Thr Glu Pro His Pro Asp Gly Ala Gly Val Ile>				

FIGURE 4
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1050	1060	1070	1080	1090
CTC TGC ATA GAG AAG GCT TTG GCT CAG TCA GGA GTC TCT AGG GAA GAC				
Leu Cys Ile Glu Lys Ala Leu Ala Gln Ser Gly Val Ser Arg Glu Asp>				
1100	1110	1120	1130	1140
GTA AAT TAC ATA AAT GCA CAT GCC ACA TCC ACT CCA GCT GGA GAT ATC				
Val Asn Tyr Ile Asn Ala His Ala Thr Ser Thr Pro Ala Gly Asp Ile>				
1150	1160	1170	1180	
AAA GAG TAC CAA GCT CTT ATC CAC TGT TTC GGC CAA AAC AAC GAG TTA				
Lys Glu Tyr Gln Ala Leu Ile His Cys Phe Gly Gln Asn Asn Glu Leu>				
1190	1200	1210	1220	1230
AAA GTG AAT TCT ACC AAA TCA ATG ATT GGT CAC CTT CTC GGA GCA GCC				
Lys Val Asn Ser Thr Lys Ser Met Ile Gly His Leu Leu Gly Ala Ala>				
1240	1250	1260	1270	1280
GGT GGT GTG GAA GCA GTT TCA GTA GTT CAG GCA ATA AGG ACT GGG TGG				
Gly Gly Val Glu Ala Val Ser Val Val Gln Ala Ile Arg Thr Gly Trp>				
1290	1300	1310	1320	1330
ATC CAT CCG AAT ATT AAT TTG GAA AAC CCA GAT GAA GGC GTG GAT ACC				
Ile His Pro Asn Ile Asn Leu Glu Asn Pro Asp Glu Gly Val Asp Thr>				
1340	1350	1360	1370	1380
AAA TTG CTC GTG GGC CCT AAG AAG GAG AGA CTG AAC ATT AAG GTC GGT				
Lys Leu Leu Val Gly Pro Lys Lys Glu Arg Leu Asn Ile Lys Val Gly>				

FIGURE 4
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1390	1400	1410	1420
TTG TCT AAT TCA TTC GGG TTT GGT GGG CAC AAC TCG TCC ATA CTC TTC			
Leu Ser Asn Ser Phe Gly Phe Gly Gly His Asn Ser Ser Ile Leu Phe>			
1430	1440	1450	1460
			1470
			1480
GCC CCT TAC AAC TAG GCGGTTT CATGTGTGGA ATTCTACTCA ATCTATCANA			
Ala Pro Tyr Asn ***>			
1490	1500	1510	1520
	*		1530
			1540
GCTGAAGTTT TGAGGACTCC AGCATGTTGG TAGCTCCTTA CGTCTCTAGA CATGCCCATG			
1550	1560	1570	1580
	*		1590
			1600
AGTTTGTGT CGGGAGCTGT AGTCGGAACC ATGACGGATT GAGTACTCAT GCGACACAG			
1610	1620	1630	1640
	*		1650
			1660
GATATACTCC TTGCTAGAAAT TGTTAGAGCA CTATTCAATTA TCCCATTTT TTTCTGAAAT			
1670	1680	1690	1700
	*		1710
			1720
CTCCCTCCTT ACGGTAGTTG TACTTTTCGAG CGTTTCATCG AGTCAGTGAA GAAGAGAACAA			
1730	1740	1750	1760
	*		1770
			1780
AAGCTAACTC GGGCAGGTAG TAACCATTTG CCCTTTGTAT TGCTCTCTAT TTTATCGCCG			
1790	1800	1810	1820
	*		1830
			1840
TTTGTGGGT TAAATTTGT AAAACTAGAC GACTGGTTTG TTTTCTCTTG ATCATTTGGAG			

FIGURE 4
5/6

1850	1860	1870	1880	1890	1900
ATGTATGGCC	ATATTGGCT *	TTCATTGATG	ATAAAAAAAAA	AAAAAAAAA	AAAAAAAAA
1910	1920				
AAAAAAAAA	AAAAAAAAA *				
AAAAAAAAA	AAAAAAAAA				

FIGURE 4
6/6

CTGGTACGCC	TGCAGGTACC	GGTCCGGGAT	TCCCGGGTCG	ACCCACGGGT	CCGTCTTCCC	60
ACTCCGATCG	TTCCTCTTCC	ACCGCACTC	TTCCTCTCTC	TGGGCTCTC	CGCCATCCTC	120
CGCCGCC	ATG CAT	TCC CTC	CAG TCA	CCC TCC	CTT CGG	GCC TCC
	Met His	Ser Leu	Gln Ser	Pro Ser	Leu Arg	Ala Ser
	1	5	10	15	20	25
GAC CCC	TTC CGC	CCC AAA	TCA TCC	ACC GTC	CGC CCC	CTC CAC
Asp Pro	Phe Arg	Pro Lys	Ser Ser	Thr Val	Arg Pro	Leu His
15	20	25	30	35	40	45
TCA ATT	CCC AAC	GTC CGG	GCC GCT	TCC CCC	ACC GTC	TCC GCT
Ser Ile	Pro Asn	Val Arg	Ala Ala	Ser Pro	Thr Val	Ser Ala
	35	40	45	50	55	60
CGC GAG	ACC GAC	CCC AAG	AAG CGC	GTC ATC	ACC GGA	ATG GGC
Arg Glu	Thr Asp	Pro Lys	Lys Arg	Val Val	Ile Thr	Gly Met
	50	55	60	65	70	75
GTC TCC	GTT TTC	GCG TCC	GAC GTC	GAT GCG	TAC TAC	GAC AAG
Val Ser	Val Phe	Gly Ser	Asp Val	Asp Ala	Tyr Tyr	Asp Lys
	65	70	75	80	85	90
TCA GGC	GAG AGC	GGG ATC	GGC CCA	ATC GAC	CGC TTC	GAC GCC
Ser Gly	Glu Ser	Gly Ile	Gly Ile	Asp Pro	Ile Asp	Arg Phe
	80	85	90	95	100	105
TTC CCC	ACC AGG	TTC GGC	GGC CAG	ATT CGT	GGC TTC	AAC TCC
Phe Pro	Thr Arg	Phe Gly	Gly Gln	Ile Arg	Gly Phe	Asn Ser
95	100	105	110	115	120	125
TAC ATT	GAC GGC	AAA AAC	GAC AGG	CGG CTT	GAT TGC	CTT CGC
Tyr Ile	Asp Gly	Lys Asn	Asp Arg	Arg Leu	Asp Cys	Leu Arg
	115	120	125	130	135	140

FIGURE 5
1/4

TGC ATT GTC GCC GGG AAG AAG TCT CTT GAG GAC GCC GAT CTC GGT GCC 553
 Cys Ile Val Ala Gly Lys Lys Ser Leu Glu Asp Ala Asp Leu Gly Ala
 130 135 140
 GAC CGC CTC TCC AAG ATC GAC AAG GAG AGA GCC GGA CTG GTT GGG 601
 Asp Arg Leu Ser Lys Ile Asp Lys Glu Arg Ala Gly Val Leu Val Gly
 145 150 155
 ACA GGA ATG GGT GGT CTG ACT GTC TTC TCT GAC GGG GTT CAA TCT CTT 649
 Thr Gly Met Gly Gly Leu Thr Val Phe Ser Asp Gly Val Gln Ser Leu
 160 165 170
 ATC GAG AAG GGT CAC CGG AAA ATC ACC CCT TTC TTC ATC CCC TAT GCC 697
 Ile Glu Lys Gly His Arg Lys Ile Thr Pro Phe Phe Ile Pro Tyr Ala
 175 180 185 190
 ATT ACA AAC ATG GGG TCT GCC CTG CTC GCT ATT GAA CTC GGT CTG ATG 745
 Ile Thr Asn Met Gly Ser Ala Leu Leu Ala Ile Glu Leu Gly Leu Met
 195 200 205
 GGC CCA AAC TAT TCA ATT TCC ACT GCA TGT GCC ACT TCC AAC TAC TGC 793
 Gly Pro Asn Tyr Ser Ile Ser Thr Ala Cys Ala Thr Ser Asn Tyr Cys
 210 215 220
 TTC CAT GCT GCT AAT CAT ATC CGC CGT GGT GAG GCT GAT CTT ATG 841
 Phe His Ala Ala Asn His Ile Arg Arg Gly Glu Ala Asp Leu Met
 225 230 235
 ATT GCT GGA GGC ACT GAG GCC GCA ATC CCA ATT GCG TTG GGA GGC 889
 Ile Ala Gly Gly Thr Glu Ala Ala Ile Ile Pro Ile Gly Leu Gly Gly
 240 245 250

FIGURE 5
2/4

TTT GTG GCT TGC AGG GCT CTG TCT CAA AGG AAC GAT GAC CCT CAG ACT	937
Phe Val Ala Cys Arg Ala Leu Ser Gln Arg Asn Asp Pro Gln Thr	270
255	
GCC TCT AGG CCC TGG GAT AAA GAC CGT GAT GGT TTT GTG ATG GGT GAA	985
Ala Ser Arg Pro Trp Asp Lys Asp Arg Asp Gly Phe Val Met Gly Glu	285
275	
GGT GCT GGA GTG TTG GTG CTG GAG AGC TTG GAA CAT GCA ATG AAA CGA	1033
Gly Ala Gly Val Leu Val Leu Glu Ser Leu Glu His Ala Met Lys Arg	300
290	
GGA GCA CCT ATT ATT GCA GAG TAT TTG GGA GGT GCA ATC AAC TGT GAT	1081
Gly Ala Pro Ile Ile Ala Glu Tyr Leu Gly Gly Ala Ile Asn Cys Asp	315
305	
GCT TAT CAC ATG ACT GAC CCA AGG GCT GAT GGT CTC GGT GTC TCC TCT	1129
Ala Tyr His Met Thr Asp Pro Arg Ala Asp Gly Leu Gly Val Ser Ser	330
320	
TGC ATT GAG AGT AGC CTT GAA GAT GCT GGC GTC TCA CCT GAA GAG GTC	1176
Cys Ile Glu Ser Ser Leu Glu Asp Ala Gly Val Ser Pro Glu Glu Val	350
335	
AAT TAC ATA AAT GCT CAT CAT GCG ACT TCT ACT CTA GCT GGG GAT CTC GCC	1224
Asn Tyr Ile Asn Ala His Ala Thr Ser Thr Leu Ala Gly Asp Leu Ala	365
355	
GAG ATA NAT GCC ATC MAG MAG GAT TTC MAG AAC ACA MAG GAT ATC AAA	1272
Glu Ile Asn Ala Ile Lys Lys Val Phe Lys Asn Thr Lys Asp Ile Lys	380
370	

FIGURE 5
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ATT AAT GCA ACT AAG TCA ATG ATC GGA CAC TGT CTT GGA GCC TCT GGA 1320
 Ile Asn Ala Thr Lys Ser Met 390
 385
 GGT CTT GAA GCT ATA GCG ACT ATT AAG GGA ATA AAC ACC GGC TGG CTT 1368
 Gly Leu Glu Ala Ile Ala Thr Ile Lys Gly Ile Asn Thr Gly Trp Leu
 400 405 410
 CAT CCC AGC ATT AAT CAA TTC AAT CCT GAG CCA TCC GTG GAG TTC GAC 1416
 His Pro Ser Ile Asn Gln Phe Asn Pro Glu Pro Ser Val Glu Phe Asp
 415 420 425
 ACT GTT GCC AAC AAG AAG CAG CAA CAC GAA GTT AAT GTT GCG ATC TCG 1464
 Thr Val Ala Asn Lys Lys Gln Gln His Glu Val Asn Val Ala Ile Ser
 435 440 445
 AAT TCA TTT GGA TTC GGA GGC CAC AAC TCA GTC GTG GCT TTC TCG GCT 1512
 Asn Ser Phe Gly Phe Gly Gly His Asn Ser Val Val Ala Phe Ser Ala
 450 455 460
 TTC AAG CCA TGA TTACC CATTTTCACAA GGCACCTGTGTC ATTGAGAGAGTA CCGTTGTTTCG 1569
 Phe Lys Pro 465
 TCAAAACCCCAT TTAGGATACCT GTTCTATGTA AAAAAAAGTA AGGATTATCA CTTTCCCTTC 1629
 TAATCCTGTC TCCAGTTTGA GAATGAAATT ATATTTTATTT TAAAAAANA AAAAAAGGGC 1689
 GGCCGCTCTA GAGGATCCAA GCT 1712

FIGURE 5
 4/4

Sequence Range: 1 to 1802

10	20	30	40	50	60
GGTCGACCCA CGCGTCCGGG CTTTCCGACC ACATTTCAAT TCTTGCCFCG TTTATCTCCGC					
70	80	90	100	110	
CGCTCCTCCG	CCGTGCTTCG	CCGCCGCCGC	C ATG CAA TCC	CTC CAC TCC	CCT TCC
			Met Gln Ser	Leu His Ser	Pro Ser
120	130	140	150	160	
CTC CGC CCC	TCC CCT CTC	GAG CCC TTC	CGC CTC AAT	TCC CCC	TCC TCC
Leu Arg Pro	Ser Pro Leu	Glu Pro Phe	Arg Leu Asn	Ser Pro Ser	Ser
170	180	190	200	210	
GCC GCC GCT	CTC CGC CCC	CGT CGC GCC	AGC CTC CCC	GTC ATC	CGT
Ala Ala Ala	Leu Arg Pro	Leu Arg Ala	Ser Leu Pro	Val Ile Arg	
220	230	240	250		
GCT GCC ACC	GCC TCC GCC	CCC AAG	CGC GAG TCC	GAC CCC	AAG AAG CGG
Ala Ala Thr	Ala Ser Ala	Pro Lys	Arg Glu Ser	Asp Pro	Lys Lys Arg
260	270	280	290	300	
GTC GTC ATC	ACC GGC ATG	GGC CTC GTC	GTC TCC	GGC TCC	GAC GTC
Val Val Ile	Thr Gly Met	Gly Leu Val	Ser Val Phe	Gly Ser	Asp Val
310	320	330	340	350	
GAC GCC TAC	TAC GAC AAG	CTG CTC TCC	GGC GAG	AGC GGC	ATC AGC CTA
Asp Ala Tyr	Tyr Asp Lys	Leu Leu Ser	Gly Glu Ser	Gly Ile Ser	Leu

FIGURE 6
1/5

360	370	380	390	400
ATC GAC CGC TTC GAC GCT TCC AAA TTC CCC ACC AGG TTC GCC GGC CAG				
Ile Asp Arg Phe Asp Ala Ser Lys Phe Pro Thr Arg Phe Ala Gly Gln				
410	420	430	440	450
ATC CGT GGC TTC AAC GCG ACG GGC TAC ATC GAC GGC AAG AAC GAC CCG				
Ile Arg Gly Phe Asn Ala Thr Gly Tyr Ile Asp Gly Lys Asn Asp Arg				
460	470	480	490	
CGG CTC GAC GAT TGC CTC CGC TAC TGC ATT GTC GCC GGC AAG AAG GCT				
Arg Leu Asp Asp Cys Leu Arg Tyr Cys Ile Val Ala Gly Lys Lys Ala				
500	510	520	530	540
CTC GAA GAC GCC GAT CTC GCC GGC CAA TCC CTC TCC AAG ATT GAT AAG				
Leu Glu Asp Ala Asp Leu Ala Gly Gln Ser Leu Ser Lys Ile Asp Lys				
550	560	570	580	590
GAG AAG GCC GGA GTG CTA GTT GGA ACC GGT ATG GGT GGC CTA ACT GTC				
Glu Arg Ala Gly Val Leu Val Gly Thr Gly Met Gly Gly Leu Thr Val				
600	610	620	630	640
TTC TCT GAC GGG GTT CAG AAT CTC ATC GAG AAA GGT CAC CGG AAG ATC				
Phe Ser Asp Gly Val Gln Asn Leu Ile Glu Lys Gly His Arg Lys Ile				
650	660	670	680	690
TCC CCG TTT TTC ATT CCA TAT GCC AAT ACA AAC ATG GGG TCT GCG CTG				
Ser Pro Phe Phe Ile Pro Tyr Ala Ile Thr Asn Met Gly Ser Ala Leu				

FIGURE 6
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700	710	720	730
CTT GCC ATC GAT TTG GGT CAG ATG GGC CCA AAC TAT TCG ATT TCA ACT			
Leu Ala Ile Asp Leu Gly Leu Met Gly Pro Asn Tyr Ser Ile Ser Thr			
740	750	760	770
			780
GCA TGT GCT ACT TCC AAC TAC TGC TTT TAT GCT GCC GGC AAT CAT ATC			
Ala Cys Ala Thr Ser Asn Tyr Cys Phe Tyr Ala Ala Asn His Ile			
790	800	810	820
			830
CGC CGA GGT GAG GCT GAC CTG ATG ATT GCT GGA GGA ACT GAG GCT GCG			
Arg Arg Gly Glu Ala Asp Leu Met Ile Ala Gly Gly Thr Glu Ala Ala			
840	850	860	870
			880
GTC AAT CCA ATT GGT TTA GGA GGA TTC GAT GCC TGC AGG GCT TTA TCT			
Val Ile Pro Ile Gly Leu Gly Gly Phe Val Ala Cys Arg Ala Leu Ser			
890	900	910	920
			930
CAA AGG AAT GAT GAT CCT CAG ACT GCC TCA AGG CCG TGG GAT AAG GAC			
Gln Arg Asn Asp Asp Pro Gln Thr Ala Ser Arg Pro Trp Asp Lys Asp			
940	950	960	970
CGT GAT GGC TTT GTG ATG GGT GAA GGG GCT GGA GTA TTG GTT ATG GAG			
Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Val Met Glu			
980	990	1000	1010
			1020
AGC TTG GAG CAT GCA ATG AAA CGG GGA CCG CCG AAT ATT GCA GAA TAT			
Ser Leu Glu His Ala Met Lys Arg Gly Ala Pro Ile Ile Ala Glu Tyr			

FIGURE 6

1030	1040	1050	1060	1070
TTG GGA GGT GCA GTC AAC TGT GAT GCT TAT CAT ATG ACT GAT CCA AGG				
Leu Gly Gly Ala Val Asn Cys Asp Ala Tyr His Met Thr Asp Pro Arg				
1080	1090	1100	1110	1120
GCT GAT GGG CTT GGT GTC TCC TCG TGC ATT GAG AGC AGT CTC GAA GAT				
Ala Asp Gly Leu Gly Val Ser Ser Cys Ile Glu Ser Ser Leu Glu Asp				
1130	1140	1150	1160	1170
GCC GGG GTC TCA CCT GAA GAG GTC AAT TAC ATA AAT GCT CAT GCG ACT				
Ala Gly Val Ser Pro Glu Glu Val Asn Tyr Ile Asn Ala His Ala Thr				
1180	1190	1200	1210	
TCT ACT CTT GCT GGG GAT CTT GCC GAG ATA AAT GCC ATT AAG AAA GTT				
Ser Thr Leu Ala Gly Asp Leu Ala Glu Ile Asn Ala Ile Lys Lys Val				
1220	1230	1240	1250	1260
TTC AAG AAC ACC AAG GAA ATC AAA ATC AAT GCA ACT AAG TCA ATG ATC				
Phe Lys Asn Thr Lys Glu Ile Lys Ile Asn Ala Thr Lys Ser Met Ile				
1270	1280	1290	1300	1310
GGA CAC TGT CTT GGA GCA TCA GGA GGT CTT GAA GCC ATC GCA ACC ATT				
Gly His Cys Leu Gly Ala Ser Gly Gly Leu Glu Ala Ile Ala Thr Ile				
1320	1330	1340	1350	1360
AAG GGA ATA ACC ACC GGC TGG CTT CAT CCC AGC AAT CAA TTT AAT				
Lys Gly Ile Thr Thr Gly Trp Leu His Pro Ser Ile Asn Gln Phe Asn				

FIGURE 6
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1370	1380	1390	1400	1410
CCC GAG CCA TCG GTG GAC TTC AAC ACT GGT GCC AAC AAA AAG CAG CAA				
Pro Glu Pro Ser Val Asp Phe Asn Thr Val Ala Asn Lys Lys Gln Gln				
1420	1430	1440	1450	
CAT GAA GTG AAC GTC GCT ATC TCG AAT TCT TTT GGA TTT GGA GGG CAC				
His Glu Val Asn Val Ala Ile Ser Asn Ser Phe Gly Phe Gly His				
1460	1470	1480	1490	1500
AAC TCG GTT GTG GCA TTC TCA GCT TTC AAG CCA TGA ATTCT ACTTGGTTCA				
Asn Ser Val Val Ala Phe Ser Ala Phe Lys Pro ***				
1520	1530	1540	1550	1560
AAATGCACAC CAGTTGCTGA GATAGGGCTT CAACCTGCAG AGCAATTTT TAAATGCCCTT				
1580	1590	1600	1610	1620
GTCCGGAAGAG CGTAATACCG GAATAGGTGG GTCCCTTIGAT AGTTCCTCGA AGCCATTTAG				
1640	1650	1660	1670	1680
GATGATGTTT TACTGTAAATA ATCGAAGATG ATTCCCATTT TAAATCTAGT CTCTGATTTA				
1700	1710	1720	1730	1740
TGTATTAGAA AGACCAATGA AAGATTTTGT GTCATGTTTG TGTGTCAAT GTTATTTAAG				
1760	1770	1780	1790	1800
ATAAAGCANA AAAAAAAAAA AAGGGCGGCC GCTCTAGAGG ATCCAGCTTA CTT				

FIGURE 6

Sequence Range: 1 to 2369

10	20	30	40	50	60
GTACGCCCTGC AGGTAACCGGT CCGGAATCC CGGGTCGACC CACGGGTCCG CATMAAAGAG					
70	80	90	100	110	120
AGAGAGAGGG ATCCATCGAA TCGGGCCACC CTCCTTTTCAT CTTGGAATCA TTACCATACC					
130	140	150	160	170	180
ATTCCGCCTGA TCCATTTTCC GCCATTTCGG GGTCTTTCAT CCCMAAGGGT ATCCTTTTCT					
190	200	210	220	230	
ATCCTATCTT CTCMAAGGGT CAGTCAGTTC CCTCCA ATG CCT GCC GCC TCT TCC					
Met Pro Ala Ala Ser Ser>					
240	250	260	270	280	
CTG CTC GCT TCC CCT CTC TGT ACG TGG CTC CTT GCC GCC TGC ATG TCT					
Leu Leu Ala Ser Pro Leu Cys Thr Trp Leu Leu Ala Ala Cys Met Ser>					
290	300	310	320	330	
ACC TCC TTC CAC CCC TCC GAC CCT CTT CCG CCT TCC ATC TCC TCT CCT					
Thr Ser Phe His Pro Ser Asp Pro Leu Pro Pro Ser Ile Ser Ser Pro>					
340	350	360	370		
CCC CGA CGC CTC TCC CGC CGG ATT CTC TCC CAA TGC GCC CCA CTA					
Arg Arg Arg Leu Ser Arg Arg Arg Ile Leu Ser Gln Cys Ala Pro Leu>					

FIGURE 7
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380		390	400	410	420
	CCT TCT GCT TCC TCC GCC CTC CGC GGA TCC AGT TTC CAT ACC CTC GTC				
	Pro Ser Ala Ser Ser Ala Leu Arg Gly Ser Ser Phe His Thr Leu Val>				
430		440	450	460	470
	ACC TCT TAC CTC GCC TGC TTC GAG CCC TGC CAT GAC TAC TAT ACA TCC				
	Thr Ser Tyr Leu Ala Cys Phe Glu Pro Cys His Asp Tyr Tyr Thr Ser>				
480		490	500	510	520
	GCA TCC TTG TTC GGA TCC AGA CCC ATT CGC ACC ACC CGC AGG CAC CGG				
	Ala Ser Leu Phe Gly Ser Arg Pro Ile Arg Thr Thr Arg Arg His Arg>				
530		540	550	560	570
	AGG CTC AAT CGA GCT TCC CTT TCC AGG GAG GCA ATG GCC GTG GCT CTG				
	Arg Leu Asn Arg Ala Ser Pro Ser Arg Glu Ala Met Ala Val Ala Leu>				
580		590	600	610	
	CMA CCT GMA CAG GMA GTT ACC ACA AAG AAG AAG CCA AGT ATC AAA CAG				
	Gln Pro Glu Gln Glu Val Thr Thr Lys Lys Lys Pro Ser Ile Lys Gln>				
620		630	640	650	660
	CGG CGA GTA GTT GTG ACT GGA ATG GGT GTG GTG ACT CCT CTA GGC CAT				
	Arg Arg Val Val Val Thr Gly Met Gly Val Val Thr Pro Leu Gly His>				
670		680	690	700	710
	GAC CCT GAT GTT TTC TAC AAT AAT CTG CTT GAT GGA ACG AGT GGC ATA				
	Asp Pro Asp Val Phe Tyr Asn Asn Leu Leu Asp Gly Thr Ser Gly Ile>				

FIGURE 7
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720	730	740	750	760
AGC GAG ATA GAG ACC TTT GAT TGT GCT CAA TTT CCT ACC AGA ATT GCT				
Ser Glu Ile Glu Thr Phe Asp Cys Ala Gln Phe Pro Thr Arg Ile Ala>				
770	780	790	800	810
GGA GAG ATC AAG TCT TTC TCC ACA GAT GGT TGG GTG GCC CCG AAG CTC				
Gly Glu Ile Lys Ser Phe Ser Thr Asp Gly Trp Val Ala Pro Lys Leu>				
820	830	840	850	
TCT AAG AGG ATG GAC AAG TTC ATG CTA TAC ATG CTG ACC GCT GGC AAG				
Ser Lys Arg Met Asp Lys Phe Met Leu Tyr Met Leu Thr Ala Gly Lys>				
860	870	880	890	900
AAA GCA TTA ACA GAT GGT GGA ATC ACC GAA GAT GTG ATG AAA GAG CTA				
Lys Ala Leu Thr Asp Gly Gly Ile Thr Glu Asp Val Met Lys Glu Leu>				
910	920	930	940	950
GAT AAA AGA AAA TGC GGA GTT CTC ATT GGC TCA GCA ATG GGT GGA ATG				
Asp Lys Arg Lys Cys Gly Val Leu Ile Gly Ser Ala Met Gly Gly Met>				
960	970	980	990	1000
AAG GTA TTC AAT GAT GCC ATT GAA GCC CTA AGG ATT TCA TAT AAG AAG				
Lys Val Phe Asn Asp Ala Ile Glu Ala Leu Arg Ile Ser Tyr Lys Lys>				
1010	1020	1030	1040	1050
ATG AAT CCC TTT TGT GTA CCT TTC GCT ACC ACA AAT ATG GGA TCA GCT				
Met Asn Pro Phe Cys Val Pro Phe Ala Thr Thr Asn Met Gly Ser Ala>				

FIGURE 7
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1060	1070	1080	1090
ATG CTT GCA ATG GAC TTG GGA TGG ATG GGG CCC AAC TAC TCG ATA TCT			
Met Leu Ala Met Asp Leu Gly Trp Met Gly Pro Asn Tyr Ser Ile Ser>			
1100	1110	1120	1130
			1140
ACT GCT TGT GCA ACG AGT AAC TTT TGT ATG AAT GCT GCG AAC CAT			
Thr Ala Cys Ala Thr Ser Asn Phe Cys Ile Met Asn Ala Ala Asn His>			
1150	1160	1170	1180
			1190
ATA ATC AGA GGC GAA GCA GAT GTG ATG CTT TGC GGG GGC TCA GAT GCG			
Ile Ile Arg Gly Glu Ala Asp Val Met Leu Cys Gly Gly Ser Asp Ala>			
1200	1210	1220	1230
			1240
GTA ATC ATA CCT ATT GGT ATG GGA GGT TTT GTT GCA TGC CGA GCT TTG			
Val Ile Ile Pro Ile Gly Met Gly Gly Phe Val Ala Cys Arg Ala Leu>			
1250	1260	1270	1280
			1290
TCC CAG AGA AAT TCC GAC CCT ACT AAA GCT TCA AGA CCA TGG GAC AGT			
Ser Gln Arg Asn Ser Asp Pro Thr Lys Ala Ser Arg Pro Trp Asp Ser>			
1300	1310	1320	1330
AAT CGT GAT GGA TTT GTT ATG GGG GAA GGA GCT GGA GTG CTA CTA CTA			
Asn Arg Asp Gly Phe Val Met Gly Glu Gly Ala Gly Val Leu Leu Leu>			
1340	1350	1360	1370
			1380
GAG GAG TTG GAG CAT GCA AAG AAA AGA GGT GCG ACT ATT TAC GCA GAA			
Glu Glu Leu Glu His Ala Lys Lys Arg Gly Ala Thr Ile Tyr Ala Glu>			

FIGURE 7
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1390	1400	1410	1420	1430
TTT CTA GGT GGG AGT TTC ACT TGC GAT GCC TAC CAC ATG ACC GAG CCT				
Phe Leu Gly Gly Ser Phe Thr Cys Asp Ala Tyr His Met Thr Glu Pro>				
1440	1450	1460	1470	1480
CAC CCT GAT GGA GCT GGA GTG ATT CTC TGC ATA GAG AAG GCT TTG GCT				
His Pro Asp Gly Ala Gly Val Ile Leu Cys Ile Glu Lys Ala Leu Ala>				
1490	1500	1510	1520	1530
CAG TCA GGA GTC TCT AGG GAA GAC GTA AAT TAC ATA AAT GCC CAT GCC				
Gln Ser Gly Val Ser Arg Glu Asp Val Asn Tyr Ile Asn Ala His Ala>				
1540	1550	1560	1570	
ACA TCC ACT CCG GCT GGA GAT ATC AAA GAG TAC CAA GCT CTT ATC CAC				
Thr Ser Thr Pro Ala Gly Asp Ile Lys Glu Tyr Gln Ala Leu Ile His>				
1580	1590	1600	1610	1620
TGT TTC GGC CAA AAC AGA GAG TTA AAA GTT AAT TCA ACC AAA TCA ATG				
Cys Phe Gly Gln Asn Arg Glu Leu Lys Val Asn Ser Thr Lys Ser Met>				
1630	1640	1650	1660	1670
ATT GGT CAC CTT CTC GGA GCA GCC GGT GGT GTG GAA GCA GTT TCA GTA				
Ile Gly His Leu Leu Gly Ala Ala Gly Val Glu Ala Val Ser Val>				
1680	1690	1700	1710	1720
GTT CAG GCA ATA AGG ACT GGG TGG ATC CAT CCG AAT ATT AAT TTG GAA				
Val Gln Ala Ile Arg Thr Gly Trp Ile His Pro Asn Ile Asn Leu Glu>				

FIGURE 7
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1730	1740	1750	1760	1770
AAC CCA GAT GAA GGC GTG GAT ACA AAA TTG CTC GTG GGT CCT AAG AAG				
Asn Pro Asp Glu Gly Val Asp Thr Lys Leu Ser Asn Ser Phe Gly Phe Lys>				
1780	1790	1800	1810	
GAG AGA CTG AAC GTT MAG GTC GG'T T'IG TCT' ANT' TCA TTT' GGG TTT' GGT				
Glu Arg Leu Asn Val Lys Val Gly Val Gly Leu Ser Asn Ser Phe Gly Phe Gly>				
1820	1830	1840	1850	1860
GGG CAC AAC TCG TCC ATA CTC TTC GCC CCT' TAC ATC TAG GAC GTTTCCTGT				
Gly His Asn Ser Ser Ile Leu Phe Ala Pro Tyr Ile ***>				
1880	1890	1900	1910	1920
GTGGAAATTCT ACTCAACATA TCAAAAGCTGA AGTTTGGAG ACTCCAGCAT' GTTGGTAGCT				
1940	1950	1960	1970	1980
CCTTACGCT CTAGACATGC CCATGAGTTT TGTGTCCGGA GCTTTAGTCG GAACCATGAC				
2000	2010	2020	2030	2040
GGATTGAGTA CTCATGCCGA CACTTGATAT ACTCCITGCT AGAATTGTTG GTAGAGCAAT				
2060	2070	2080	2090	2100
ATTCAATTATC TCATATTTT'T TTTTCTCTG AAATCTCCCT CCTTGGCAATA GTTGTACTTT				
2120	2130	2140	2150	2160
CGAGCTTTTC ATCGAGTCAG TGMAGMAGAG AACAAAGCTG TTAACTCGGG CACG'TAGTAA				

FIGURE 7
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2180	2190	2200	2210	2220	2230
CCATTGGCC	TTTGTTTTTC	TCTCTATTTC	ATCACCCTTT	TGTGGTTTTA	AAATTGTAA
2240	2250	2260	2270	2280	2290
AACTAGNAGA	CTGGTTTAGA	TGGTTTGT	TTCTCATTGA	TAAATTGGGGR	ATGATATGTT
2300	2310	2320	2330	2340	2350
TGGAAATATA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA
2360	AGGGCGGCCG CTCTAGAGG				

FIGURE 7
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Sequence Range: 1 to 2374

```
10      20      30      40      50      60
-A-CNTGGTC CGGAATTCCC GGGTCGACCC ACGCGTCCGC GACGCCAACC CACACCAAC
70      80      90     100     110     120
TTCCTCAGCT TCTCTCTCA AGACGGACGC CATTGGCAGC AGACAGACAG ACAGACAGAC
130     140     150     160     170     180
CCATAAAGA GAGAGAGAGG GATCCATCGA ATGCGGCCAC CCTCCCTTCA TCTTCGATTTC
190     200     210     220     230     240
ATTACCATAC CATTCCGGCTG ATCCATTTC CCGCTTTTCC GGGTCTTTCA TCCCAAGGG
250     260     270     280     290     300
TATCCTTTTC TATCCATATCT TCTCAAGGG TCAGTCAGTT CCCTCCCATG CCTGCCGCCT
310     320     330     340     350     360
CTTCCCTGCT CGCTTCCCTCT CTCTGTAGGT GGTCTCTTGC CGCTTGCATG TCTACCTCCT
370     380     390     400     410     420
TCCACCCCTC CGACCCCTCTT CCGCCATTCCA TCTCCTCTCC TCGCCGACGC CTCTCCCGCC
430     440     450     460     470     480
GCCGGATTCT CTCCCAATGC GCCCCACTAC CTTCTGCTTC CTCCGCCCTC CGCGGATCCA
```

FIGURE 8
1/5

490	500	510	520	530	540
GTTTCCATAC	CCTCGTACCC	TCTTACCCTCG	CC'TGCTTCGA	GCCCTGCCAT	GACTACTATA
550	560	570	580	590	600
CATCCGCATC	C'TGT'TCGGA	TCCAGACCCCA	T'ICGCACCAC	CCGCAGGCAC	CGGAGGCTCA
610	620	630	640	650	660
ATCGAGCTTC	CCCTTCCAGG	GGAGGCCAATG	GCCGTGGCTC	TGCNACCCTGA	ACAGGMAGT'T
670	680	690	700	710	720
ACCACAAAGA	AGAAGCCCAAG	TATCNAAACAG	CGGCGAGTAG	T'GTGAC'TGG	AA'TGGGTGTG
730	740	750	760	770	780
GTGACTCCTC	TAGGCCATGA	ACCTGATGTT	T'TCTACAAAT	AA'TCTGCTTG	ATGGNACGAG
790	800	810	820	830	840
TGGCATTAAGC	GAGATAGAGA	CCTTTGAT'IG	TGCTCAAA'TT'	CCTACGAGAA	T'IGCTGGAGA
850	860	870	880	890	900
GATCAAGTCT	TTCTCCACAG	ATGGTTGGGT	GGCCCCGAAAG	CT'C'TCTAAGA	GGATGGACAA
910	920	930	940	950	960
GTTCAATGCTA	TACATGCTGA	CTGCTGGCNA	GAAGAATTA	ACAGATGGTG	GAATCACCCGA
970	980	990	1000	1010	1020
AGATGTGATG	AAAGAGCTAG	ATAAAGAAA	ATGCGGAGT'T	CTCANTGGCT	CAGCMAATGGG

FIGURE 8
2/5

1030	1040	1050	1060	1070	1080
TGGAAAGGAG	GTAATCAATG	ATGCCATAGA	AGCCCATAAG	ATTTCAATATA	AGAAGATGAA
1090	1100	1110	1120	1130	1140
TCCCATTGTG	GTACCTTTTC	CTACCACAAA	TATGGGATCA	GCATAGCTTG	CAATGGACAT
1150	1160	1170	1180	1190	1200
GGGATGGATG	GGGCCCCAAT	ACTCGATATC	TACTGCTTGT	GCAACGAGTA	ACTTTTGTAT
1210	1220	1230	1240	1250	1260
AATGAATGCT	GCGAACCATA	TATTCAGAGG	CGAAGCAGAT	GATGATGCTTT	GCGGGGGCTC
1270	1280	1290	1300	1310	1320
AGATGCGGTA	ATCATATCCTA	TTGGTATGGG	AGGTTTGTGT	GCATGCCGAG	CTTTGTCCCA
1330	1340	1350	1360	1370	1380
GAGAAATTCC	GACCCFACFA	AGCTTCAAG	ACCATGGGAC	AGTAATCGTG	ATGGATTTGT
1390	1400	1410	1420	1430	1440
TATGGGGGNA	GGAGCTGGAG	TGCTACTACT	AGAGGAGTTG	GAGCATGCAA	AGAAAAGAGG
1450	1460	1470	1480	1490	1500
TCCGACTATT	TACGCAGAAAT	TTCTAGGTGG	GAGTTTCACT	TCCGATGCCT	ACCACATGAC

FIGURE 8
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1510	1520	1530	1540	1550	1560
CGAGCCTCAC	CC'TGATGGAG	C'IGGAGT'GAT	'I'C'I'CTGCA'TA	GAGAAAGGCTT	TGGCTCAGT'C
1570	1580	1590	1600	1610	1620
AGGAG'TCTC'I'	AGGGAAAGACG	'TAAAT'P'ACAT'	AAAT'GCCCA'T'	GCCACAN'CCA	C'TCCGGC'TGG
1630	1640	1650	1660	1670	1680
AGATATCANA	GAGTACCAAG	CTCT'ATATCCA	CTGT'TTCGGC	CAAAACAGAG	AGT'TAANAAGT
1690	1700	1710	1720	1730	1740
TAA'TTCNA'CC	AAATCAATGA	TTCG'TCACCT'I'	TCTCGGAGCA	GCCGGTGGTG	TGGAAAGCAGT
1750	1760	1770	1780	1790	1800
TTCAGT'AGTT	CAGGCAATAA	GGACTGGGTG	GATCCAT'CCG	AA'TAT'TAATT	'TGGNAANCC'CC
1810	1820	1830	1840	1850	1860
AGATCAAGGC	GTGGATACAA	AAT'GCT'CGT	GGG'TCCTAAG	AAGGAGAGAC	'TGAACGTT'AA
1870	1880	1890	1900	1910	1920
GGTCGGTTTG	TC'AAAT'CAT'	'TGGG'GTTGG	TGGGCACNAC	TGG'TCCATAC	TCTTCGCCCC
1930	1940	1950	1960	1970	1980
TTACAT'CTAG	GACGTTTTCGT	GTGTGGGAATT	C'PACTCAACA	TATCAAAAGCT	GAAGTTT'TGA
1990	2000	2010	2020	2030	2040
GGAC'TCCAGC	ATGT'TGGTAG	CTCCT'T'ACGT	C'I'CTAGACAT'	GCCCN'TGAGT'	'T'T'GTGTCCG

FIGURE 8
4/5

2050	2060	2070	2080	2090	2100
GAGCTTTAGT	CGGACCATG	ACGGATTGAG	TACTCATGGC	GACACTGAT	ATACTCCTTG
2110	2120	2130	2140	2150	2160
CTTAGAATTGT	TGGTAGAGCA	ATAATCATTA	TCATCATTA	TTTTCCTC	TGAAAATCTCC
2170	2180	2190	2200	2210	2220
CTCCTTGCAA	TAGTTGTACT	TTCGAGCATT	TCATCGAGTC	AGTGAGAG	AGAACAAAGC
2230	2240	2250	2260	2270	2280
TGTTAACTCG	GGCAGGTAGT	AACCAATTGC	CCTTGTATT	GCTCTCTATT	TCATCACCGT
2290	2300	2310	2320	2330	2340
TTTGTTGGTTT	TAAAAATTGT	AAACTAGAA	GACTGGTTA	GATGGTTG	TTTTCTCAAA
2350	2360	2370			
AAAAAAAAA	AAGGGCGCC	GCCTAGAGG	ATCC		

FIGURE 8
5/5

Sequence Range: 1 to 1580

10	20	30	40	50
CCTGATTCGG	ATTCAAGAGA	GAGTTTCGTT	GCTGGG	ATG GCG AAT GCA TCT GGG
			Met Ala Asn Ala Ser Gly>	
60	70	80	90	100
TMT CTG GGT TCT TCA GTT CCF GCC C'VG AGA AGG GCA ACT CAG CAT TCG				
Phe Leu Gly Ser Ser Val Pro Ala Leu Arg Arg Ala Thr Gln His Ser>				
110	120	130	140	150
ATT TCA TCG TCT CGT GGA TCT TCC TCG GAG TTT GTC TCC AAA AGG GTG				
Ile Ser Ser Ser Arg Gly Ser Ser Ser Ser Glu Phe Val Ser Lys Arg Val>				
160	170	180	190	
TMT TGC TGT AGT GCC GTT CAG GAT TCT GAC AGG CAG TCT TTG GGT GAT				
Phe Cys Cys Ser Ala Val Gln Asp Ser Asp Arg Gln Ser Leu Gly Asp>				
200	210	220	230	240
TCT CGC TCG CCG AGG CTT GTG AGT AGA GGA TGC AAA TTA ATT GGA TCT				
Ser Arg Ser Pro Arg Leu Val Ser Arg Gly Cys Lys Leu Ile Gly Ser>				
250	260	270	280	290
GGT TCT GCT ATA CCA GCT CTT CAA GTC TCA AAT GAT GAT CTT GCT AAA				
Gly Ser Ala Ile Pro Ala Leu Gln Val Ser Asn Asp Leu Ala Lys>				
300	310	320	330	340
ATT GTC GAC ACC AAT GAT GAA TGG ATT ACT GTC CGA ACG GGG ATC CGC				
Ile Val Asp Thr Asn Asp Glu Trp Ile Thr Val Arg Thr Gly Ile Arg>				

FIGURE 9
1/5

350	360	370	380	390
AAU CGA AGG GUA CTC TCA GGU AAA GAT AGU CUA ACA AAU UUA GCA TCA				
Asn Arg Arg Val Leu Ser Gly Lys Asp Ser Leu Thr Asn Leu Ala Ser>				
400	410	420	430	
GAG GCA GCA AGG AAA GCU CUA GAG AUG GCA CAG GTA GAC GCA AAU GAU				
Glu Ala Ala Arg Lys Ala Leu Glu Met Ala Gln Val Asp Ala Asn Asp>				
440	450	460	470	480
GTG GAT AUG GTT TTG ATG TGT ACT TCT ACC CTT GAG GAC CTT TTC GGC				
Val Asp Met Val Leu Met Cys Thr Ser Thr Pro Glu Asp Leu Phe Gly>				
490	500	510	520	530
AGT GCT CCT CAG ATA TCG AAA GCA CTT GGC TGC AAA AAG AAU CCT TTG				
Ser Ala Pro Gln Ile Ser Lys Ala Leu Gly Cys Lys Lys Asn Pro Leu>				
540	550	560	570	580
TCT TAC GAC ATT ACC GCT GCA TGC AGT GCA TTT GTG TTG GGT TTA GTC				
Ser Tyr Asp Ile Thr Ala Ala Cys Ser Gly Phe Val Leu Gly Leu Val>				
590	600	610	620	630
TCA GCT GCT TGC CAC ATT AGA GGT GGG GGT TTT AAC AAU ATT CTA GTG				
Ser Ala Ala Cys His Ile Arg Gly Gly Gly Phe Asn Asn Ile Leu Val>				
640	650	660	670	
ATT GGT GCT GAT TCT CTT TCT CGG TAT GTT GAC TCG ACC GAT CGG CGA				
Ile Gly Ala Asp Ser Leu Ser Arg Tyr Val Asp Trp Thr Asp Arg Gly>				

FIGURE 9

680	690	700	710	720
ACA TGT ATT CTC TTT GGA GAT GCT GCT GGA GCT GTA GTG GTG CAG TCA				*
Thr Cys Ile Leu Phe Gly Asp Ala Ala Gly Ala Val Val Val Gln Ser>				
730	740	750	760	770
TGT GAT GCT GAG GAA GAT GGG CTC TTT GCT TTT GAT TTG CAT AGC GAT				
Cys Asp Ala Glu Glu Asp Gly Leu Phe Ala Phe Asp Leu His Ser Asp>				
780	790	800	810	820
*				
GGA GAT GGG CAA AGG CAT CTA AAA GCT GCA ATC AAA GAA GAT GAA GTT				
Gly Asp Gly Gln Arg His Leu Lys Ala Ala Ile Lys Glu Asp Glu Val>				
830	840	850	860	870
	*			
GAT AAA GCC CTG GGA CAT AAT GGG TCC ATC AGA GAT TTT CCA CCA AGG				
Asp Lys Ala Leu Gly His Asn Gly Ser Ile Arg Asp Phe Pro Pro Arg>				
880	890	900	910	
		*		
CGT TCT TCA TAC TCT TGC ATC CAA ATG AAC GGT AAA GAG GTA TTC CGC				
Arg Ser Ser Tyr Ser Cys Ile Gln Met Asn Gly Lys Glu Val Phe Arg>				
920	930	940	950	960
				*
TTT GCT TGC CGC TCT GTG CCT CAG TCA ATC GAA TCA GCA CTT GGA AAG				
Phe Ala Cys Arg Ser Val Pro Gln Ser Ile Glu Ser Ala Leu Gly Lys>				
970	980	990	1000	1010
GCC GGT CTT AAT GGA TCC AAC ATC GAC TGG TTG CTG CTT CAT CAG GCA				
Ala Gly Leu Asn Gly Ser Asn Ile Asp Trp Leu Leu His Gln Ala>				

FIGURE 9

1020	1030	1040	1050	1060
AAU CAG AGG ATC AUU GAT GCA GTA GCA ACA CGU CUA GAG GTT CCT CAA				
Asn Gln Arg Ile Ile Asp Ala Val Ala Thr Arg Leu Glu Val Pro Gln>				
1070	1080	1090	1100	1110
GAA CGA AUU ATC UCA AAC UUG GCA AAU UAC GGG AAC ACT AGU GCG GCA				
Glu Arg Ile Ile Ser Asn Leu Ala Asn Tyr Gly Asn Thr Ser Ala Ala>				
1120	1130	1140	1150	
TCC AUU CCC UUG GCA CUA GAC GAA GCT GUG AGG AGU GGA AAU GTG AAG				
Ser Ile Pro Leu Ala Leu Asp Glu Ala Val Arg Ser Gly Asn Val Lys>				
1160	1170	1180	1190	1200
CCG GGT CAC GUG AUU GCA ACC GCA GGA UUU GGC GCC GGA CTC ACA TGG				
Pro Gly His Val Ile Ala Thr Ala Gly Phe Gly Ala Gly Leu Thr Trp>				
1210	1220	1230	1240	1250
GGT TCT GCT AUU ATC AGG UUG GGA UAA GACTGA GCCGAGCCAG CACUACAGCT				
Gly Ser Ala Ile Ile Arg Trp Gly ***>				
1270	1280	1290	1300	1310
TCCTCTCMAA CCGATGTTC ACGAAUUTTT GCTTCCNTGA CCANNAAAAG AAGAAGTCAG				
1330	1340	1350	1360	1370
TCTTTTATGG AGCAAGCAAC ACGACACAGAT CTTCTATCACA TTGCCCCUUTT TCGTTCGCCCT				

FIGURE 9

1390	1400	1410	1420	1430	1440
TTTCCATTAG TTTGATGATT TTGCTGACAA TACAAATACCC ATAGTTTCTT TTGTCCTCCCAA					
1450	1460	1470	1480	1490	1500
TAAGTTATTT GTTCTCTGTT TAAATGTTCA GCCTTTACTT CATTTTGTCT CGGGACATTTG					
1510	1520	1530	1540	1550	1560
GAGATGACAG CATAAACATC ATGTTTATAT TTGCTAATAA AAAAAAAAAA AAAAAAAAAA					
1570	1580				
AAAAAAAAAA AAAAAAAAAA					

FIGURE 9
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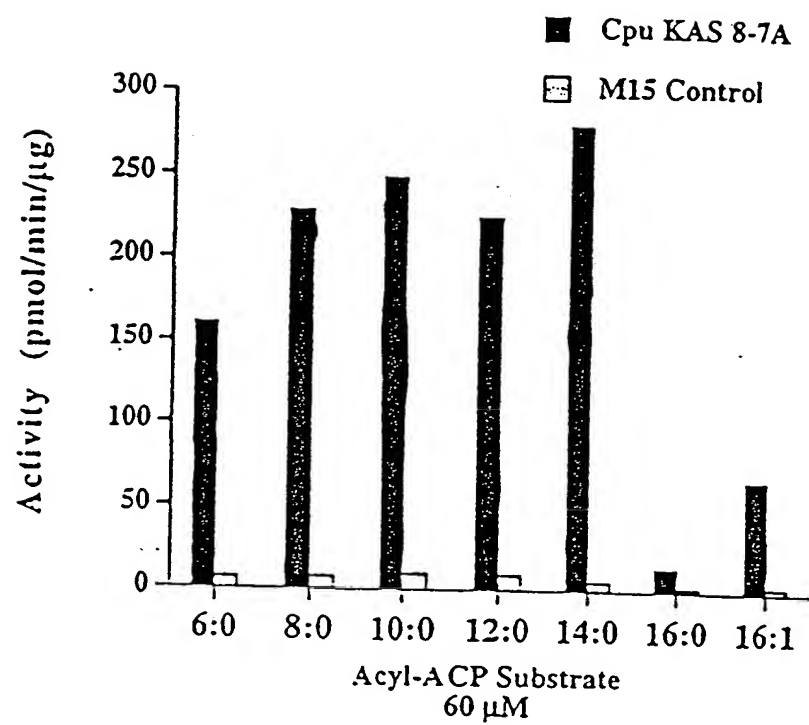


FIGURE 10

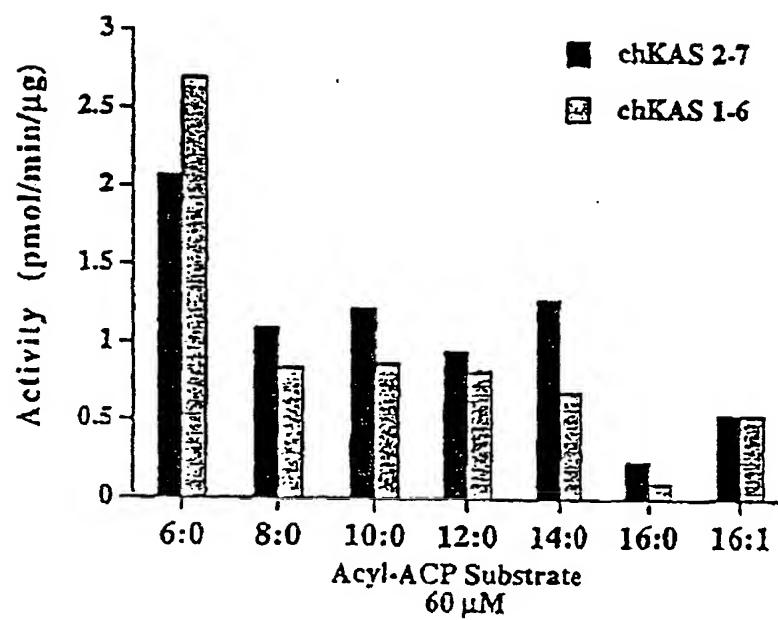


FIGURE 11

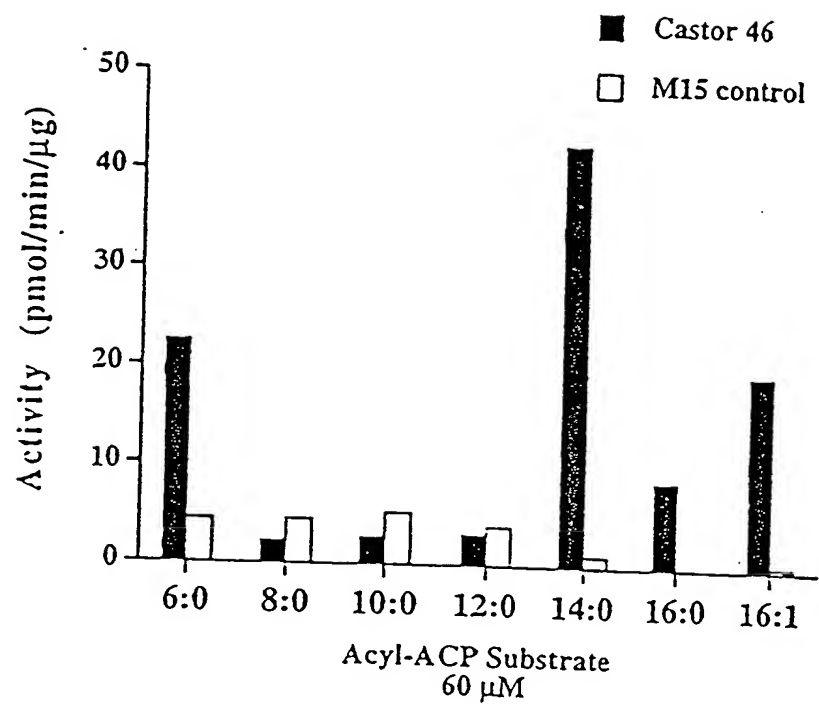
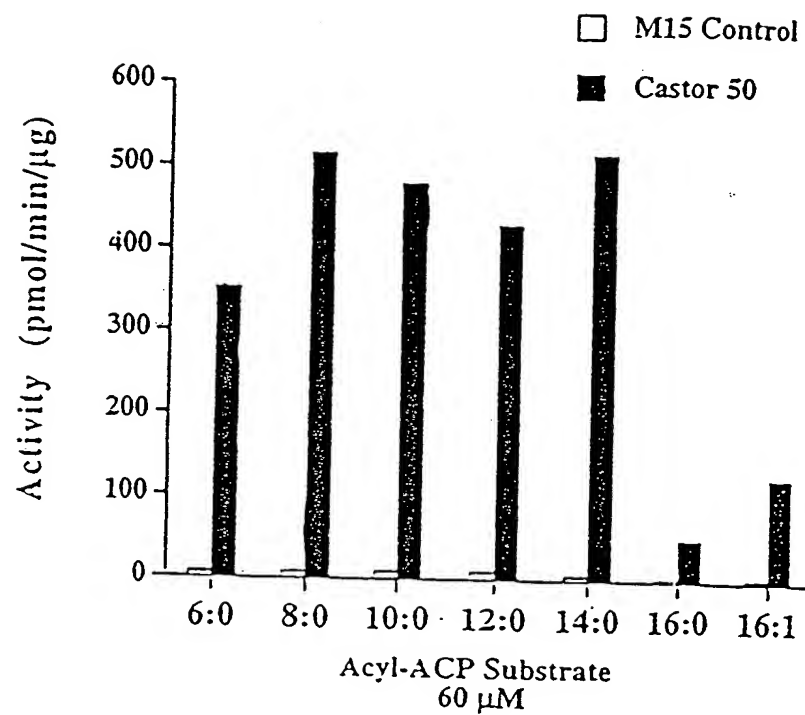


FIGURE 12



E328013-28

FIGURE 13

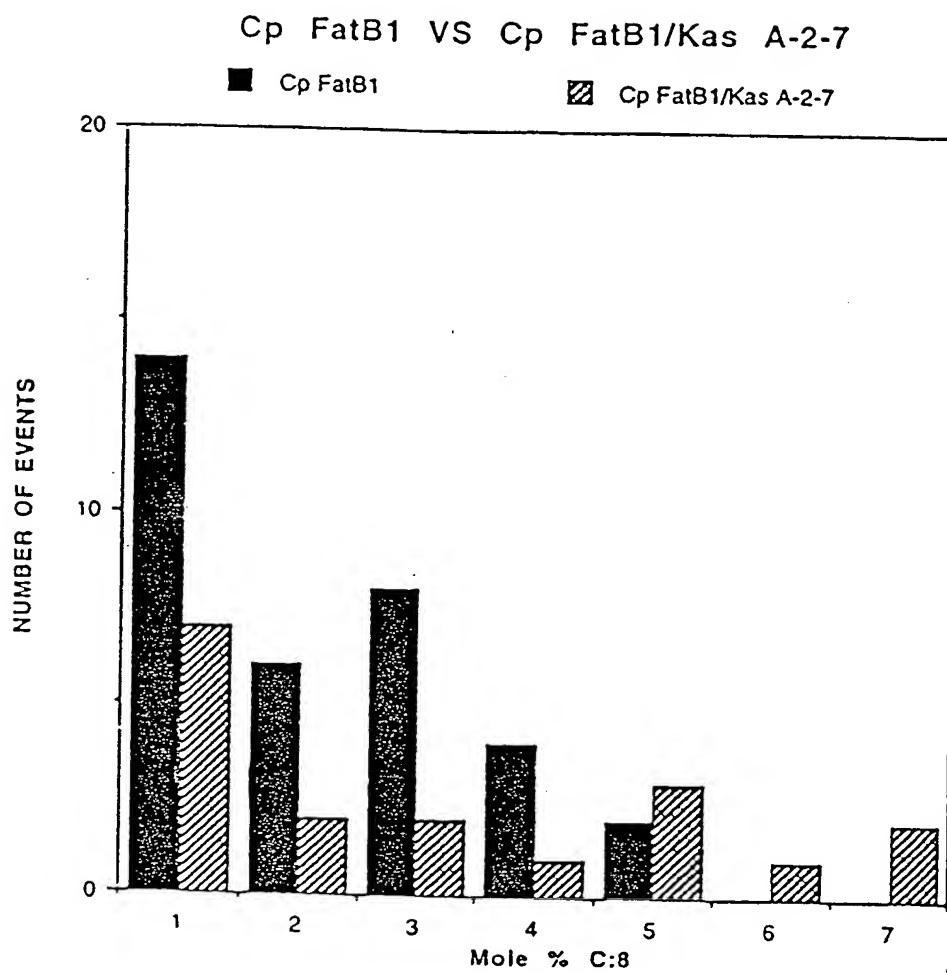


FIGURE 14

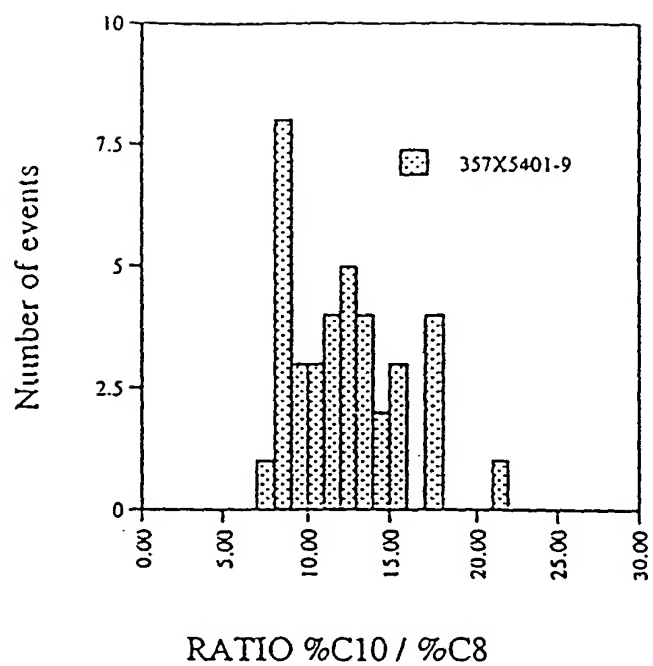


FIGURE 15A

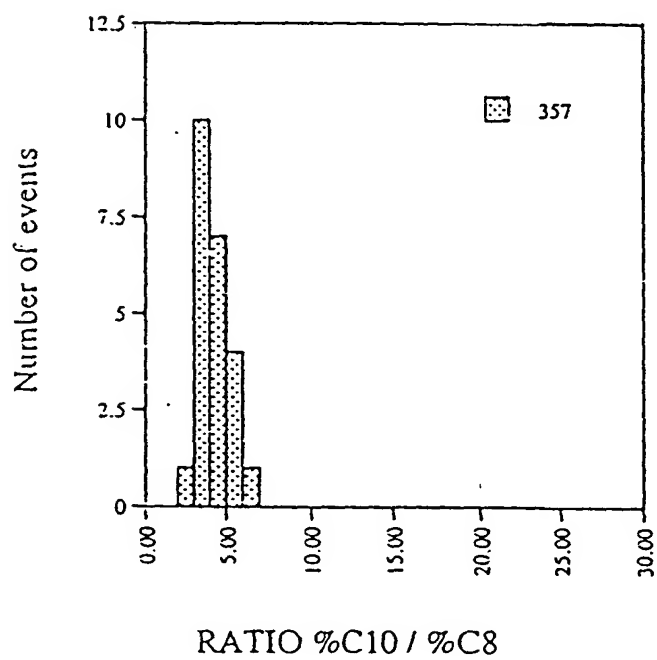


FIGURE 15B

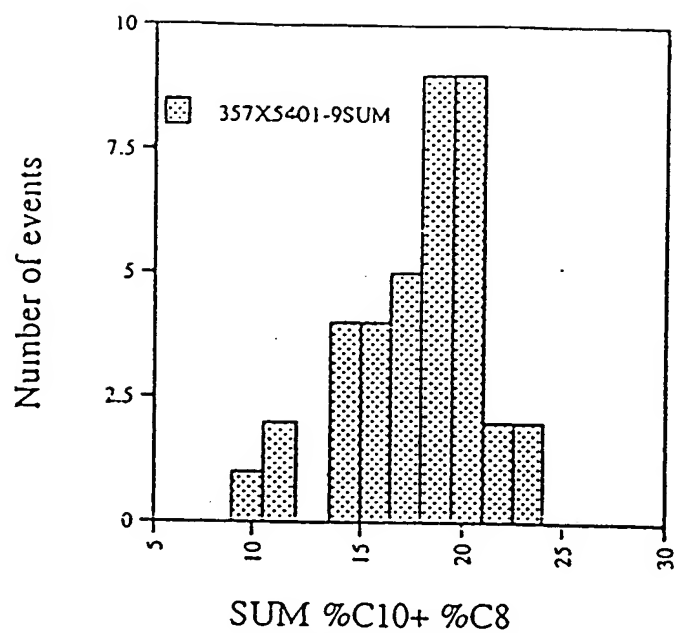


FIGURE 16A

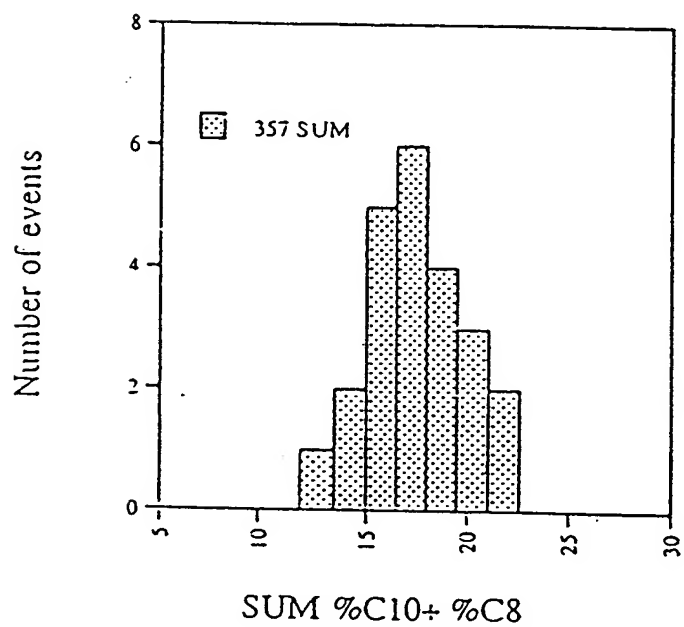
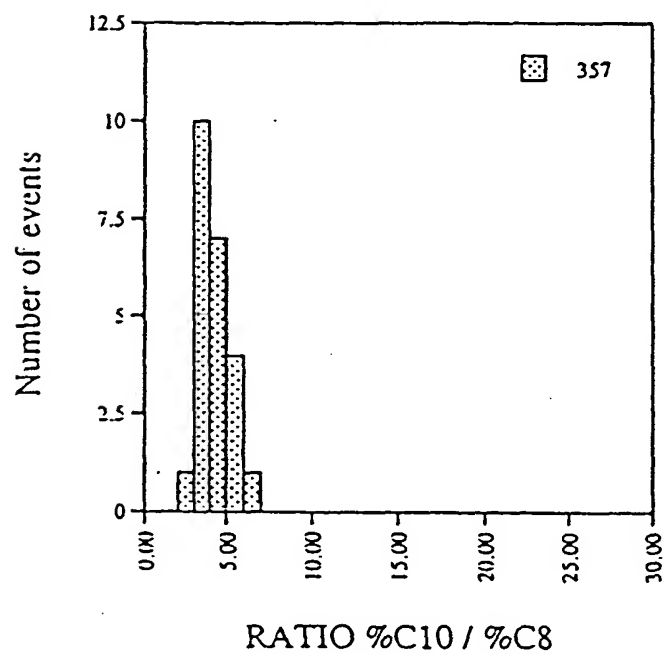
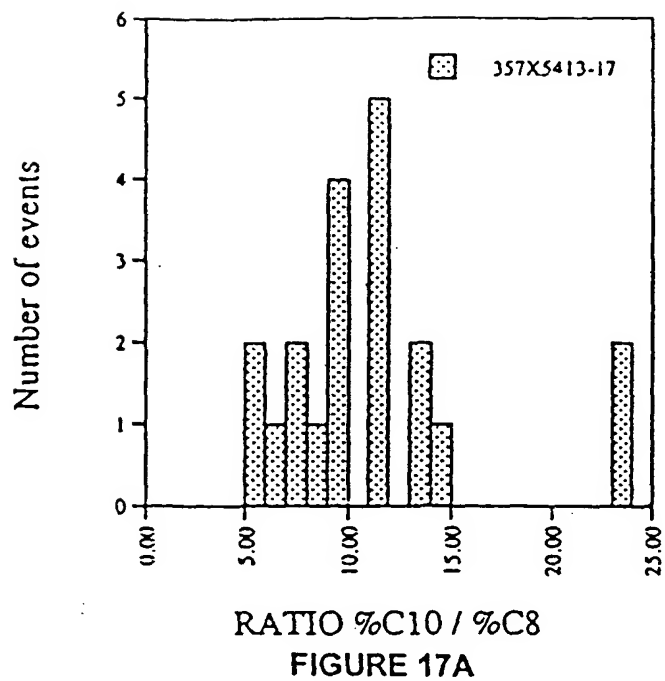


FIGURE 16B



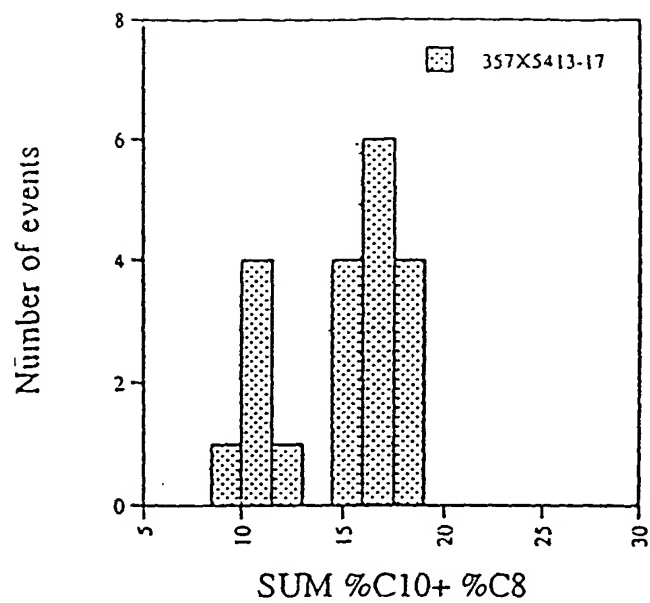


FIGURE 18A

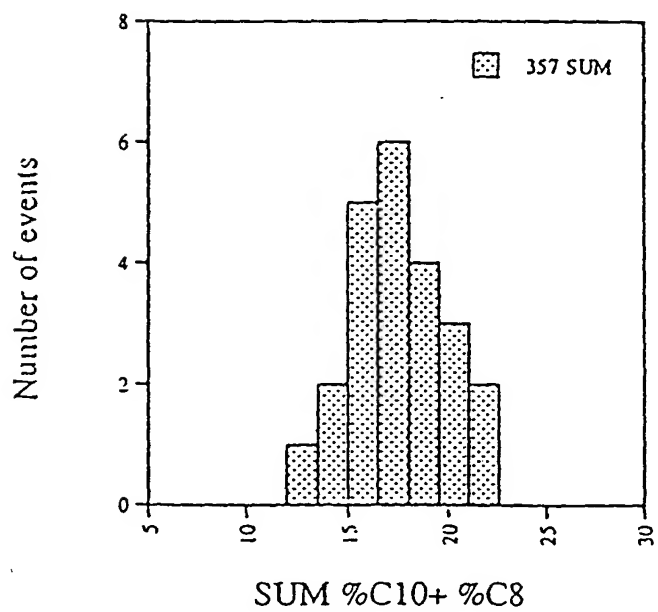


FIGURE 18B

Number of independent events

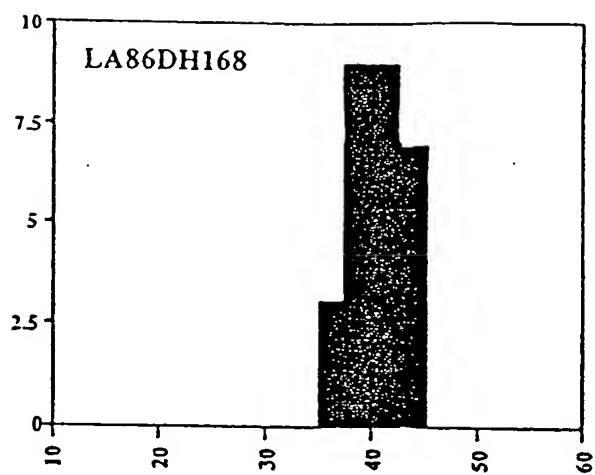


FIGURE 19A

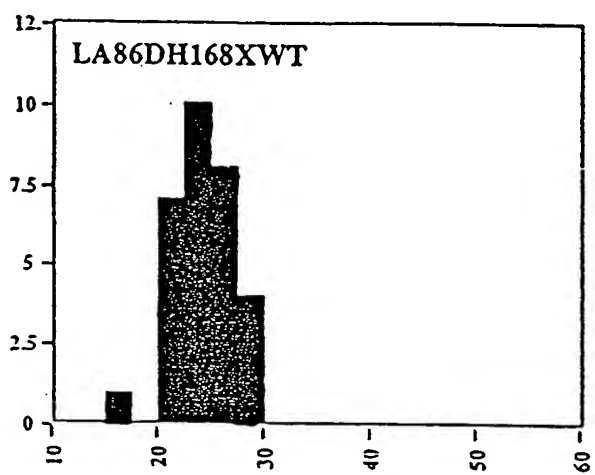


FIGURE 19B

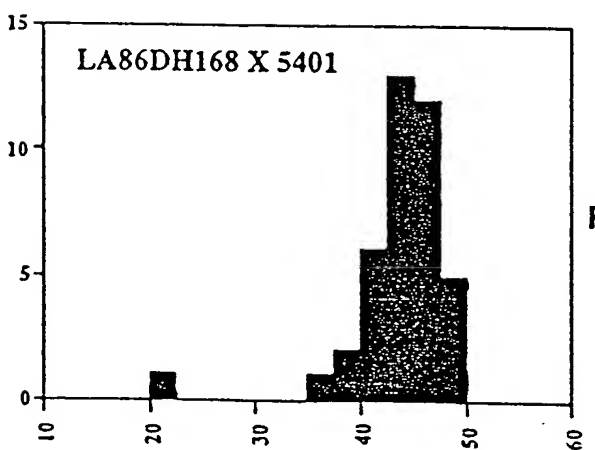


FIGURE 19BC

12:0 levels (w%)



FIGURE 20

Number of independent events

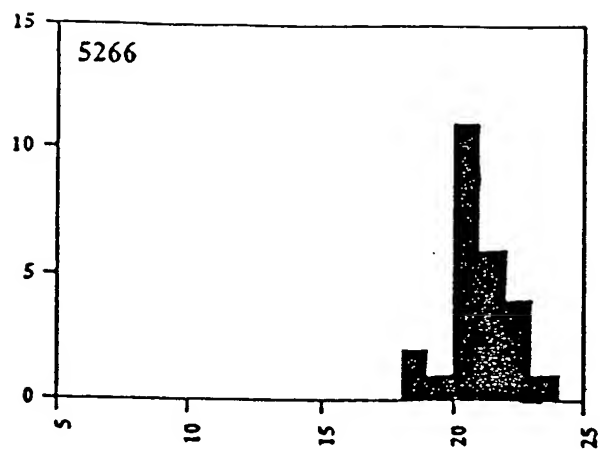


FIGURE 21A

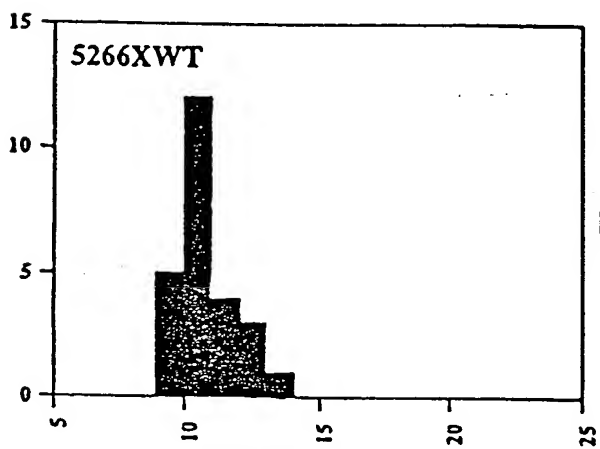


FIGURE 21B

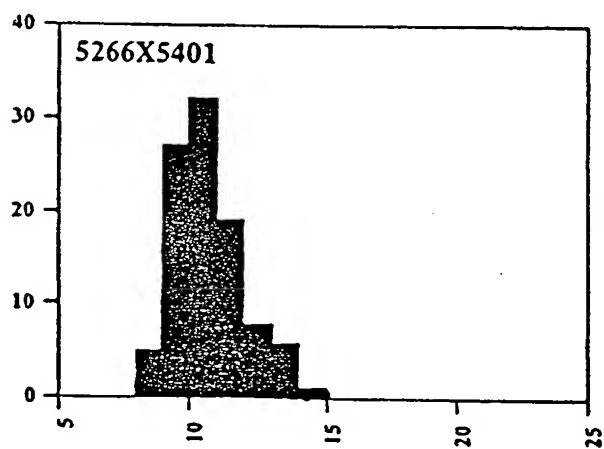


FIGURE 21C

18:0 levels (w%)

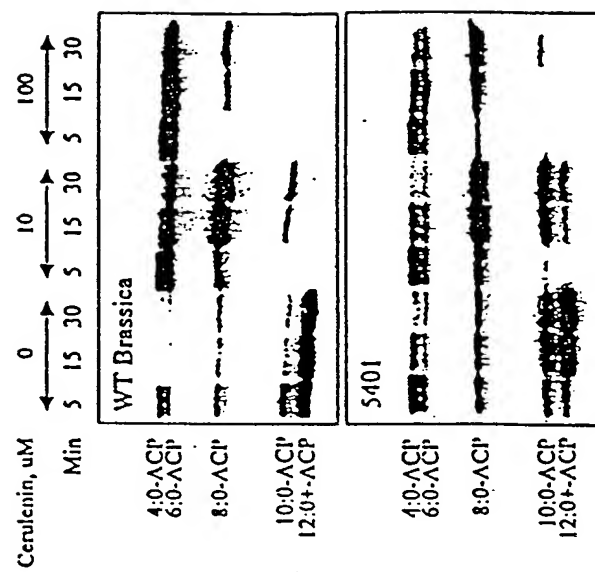


FIGURE 22